

GenCore version 5.1.6
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leic search, using sw model

April 21, 2004, 06:00:54 ; Search time 15317 Seconds
(without alignments)
11437.784 Million cell updates/sec

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Minimum Match 0%
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Listing first 45 summaries

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and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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AX001446
LOCUS AX001446
DEFINITION Sequence 1 from Patent WO9859040.
ACCESSION AX001446
VERSION AX001446.1 GI:7241612
KEYWORDS
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 4042)
AUTHORS Wick, M. and Hagen, G.
TITLE HUMAN CATALYTIC TELOMERASE SUB-UNIT AND ITS DIAGNOSTIC AN
JOURNAL THERAPEUTIC USE
Patent: WO 9859040-A 1 30-DEC-1998;

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: MARESA (DE); BAYER AG (DE)
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2888	Qy	2888	GCAGAGGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACTTC
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 HARLEY,C.B. and Andrews,W.H.
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Query Match 99.7%; Score 4028.6; DB 6; Length 4037;
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C	GAACATAGCGGTGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	727
C	GAACATAGCGGTGAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	720
C	GGCG	787
C	GGCG	780
C	CCCTGACCGCGAGCG	847
C	CCCTGACCGCGAGCG	840
C	TGGAACCGAGTGAACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	907
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C	CTCTTTGGAGGGTGGCTCTCTGCGACGCGCGCGCGCGCGCGCGCGCGCGCGCG	967
Db	901	CACCTCTTTGGAGGGTGGCTCTCTGCGACGCGCGCGCGCGCGCGCGCGCGCGCG
Qy	968	GCACCAAGCG
Db	961	GCACCAAGCG
Qy	1028	CCCGGTGTACCG
Db	1021	CCCGGTGTACCG
Qy	1088	GCCCT
Db	1081	GCCCT
Qy	1148	GACCATCTTTCTGGGTTCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
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Qy	1208	GCCCGAGCGCTACTGCGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
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Qy	1328	AGCGGCTGTCTGTGCG
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Qy	1388	CACAGACCG
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Qy	1748	TGTCACGCGAGACCG
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QY	906	GCCACCTCTTTTGAGGGGTGGCTCTCTGGCAGCGGCCACTCCACCACCCATCCGTGTG
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QY	966	CAGACCAACGCGGGCCCCCATCCACATCGCGGCCACCAACGTCCTGTGGGACACG
DB	979	CAGACCAACGCGGGCCCCCATCCACATCGCGGGCCACCAACGTCCTGTGGGACACG
QY	1026	CCCCCGGTGTACGCGAGACCAAGCACTTCTCTACTCTCCTCAGGGACAAGGAGT
DB	1039	CCCCCGGTGTACGCGAGACCAAGCACTTCTCTACTCTCCTCAGGGACAAGGAGT
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Db	2761	GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTTGGGTGGGCACGGCTTTTGT	
Qy	2828	GCGGGCCACGGGCTATTCCTGTGGTGGGCTGTCTGCTGGATATCCCGGACCTT	
Db	2821	GCGGGCCACGGGCTATTCCTGTGGTGGGCTGTCTGCTGGATATCCCGGACCTT	
Qy	2888	GCAGAGCGACTACTCCAGCTATGCCGAGCTCCATCAAGAGCCAGTCTCACTT	
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Qy	2948	CGGCTTCAGGCTGGAGGAAATGCGTGGGAACTCTTTGGGGTCTTGGCGCT	
Db	2941	CGGCTTCAGGCTGGAGGAAATGCGTGGGAACTCTTTGGGGTCTTGGCGCT	
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Db	3001	TCACAGCCTGTTTCTGGATTTGCAAGTGAAACGCTCCAGACGGTGTGCACCAA	
Qy	3068	CAAGATCTCTCTCTGACGGCTACAGGTTTACGGATGTGTGCTGACAGTCCC	
Db	3061	CAAGATCTCTCTCTGACGGCTACAGGTTTACGGATGTGTGCTGACAGTCCC	
Qy	3128	TCAGCAAGTTTGAAGAACCCCAATTTTTCTGGCGGTCATCTCTGACACGGC	
Db	3121	TCAGCAAGTTTGAAGAACCCCAATTTTTCTGGCGGTCATCTCTGACACGGC	
Qy	3188	CTGCTACTCCATCCTGAAAGCCAAAGAACGAGGATGTGCTGGGGGCCAAGGG	
Db	3181	CTGCTACTCCATCCTGAAAGCCAAAGAACGAGGATGTGCTGGGGGCCAAGGG	
Qy	3248	CGGCGCTCTGCGCTCCGAGGCGTGAGTGGCTGTGCCACCAAGCATTTCTGCT	
Db	3241	CGGCGCTCTGCGCTCCGAGGCGTGAGTGGCTGTGCCACCAAGCATTTCTGCT	
Qy	3308	GACTCGACACCGTGTCACTTCACTGTCACCTCTCTGGGGTCACTCAGGACAGCCCA	
Db	3301	GACTCGACACCGTGTCACTTCACTGTCACCTCTCTGGGGTCACTCAGGACAGCCCA	
Qy	3368	GCTGAGTCGGAAGCTCCGGGAGCAGCGTGTACTGCCCTGGAGGCGGAGGCCAA	
Db	3361	GCTGAGTCGGAAGCTCCGGGAGCAGCGTGTACTGCCCTGGAGGCGGAGGCCAA	
Qy	3428	ACTGCCCTCAGACTTCAAGACCATCTCGACTGATGGCCACCGGCCCAACAGCCA	
Db	3421	ACTGCCCTCAGACTTCAAGACCATCTCGACTGATGGCCACCGGCCCAACAGCCA	
Qy	3488	GAGCAGACACGAGGCTGTGACGCGGGCTTACAGTCCAGGAGGAGGAGGG	
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Qy	3548	CACACCGAGCCCGCACCGCTGGGAGCTGAGGCTGTAGTGAAGTCTTTGGCGCA	
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Db	2761	GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGT
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Db	3061	CAAGATCCTCTGCTGACGCGTACAGTTTACGCATGTGTGCTGCAGCTCCC
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Qy	3248	CGGCCCTCGCCTCCGAGGCCGTGAGTGGCTGTCACACCAAGCATTCCTGCT
Db	3241	CGGCCCTCGCCTCCGAGGCCGTGAGTGGCTGTCACACCAAGCATTCCTGCT
Qy	3308	GACTTCGACACCGGTGTCACTTACGTGCCATCTCTGGGGTCACTCAGGACAGCCCA
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Db	3541	CACACCCAGCCCGCACCGCTGGGAGTCTGAGGCCCTGAGTGTGTTGGCCGA
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390	
390.1 GI:27264905	
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T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,	
Y,C.B. and Andrews,W.H.	
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Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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Db	2461	CAGTGGCCCTTTTCGACGTTCTTCTACGCTTCATGTGCCACCAACGCGCGTGCAGAT
Qy	2528	CAAGTCCCTACGTCAGTGCAGGGATCCGACAGGCTCCATCTCTCTCCACGCT
Db	2521	CAAGTCCCTACGTCAGTGCAGGGATCCGACAGGCTCCATCTCTCTCCACGCT
Qy	2588	CAGCCTGTGCTACGGCGACATGAGAAACAAGCTGTTTTCGGGGATTCGCGGGGA
Db	2581	CAGCCTGTGCTACGGCGACATGAGAAACAAGCTGTTTTCGGGGATTCGCGGGGA
Qy	2648	GCTCTCGCTTTGGTGGATGATTTTCTTGTGTGTGACACCTCACTCACCCACGCG
Db	2641	GCTCTCGCTTTGGTGGATGATTTTCTTGTGTGTGACACCTCACTCACCCACGCG
Qy	2708	CTTCTCTCAGGACCCCTGGTCCGAGGTCCTCAGTATGGCTGCGTGGTGAATCTT
Db	2701	CTTCTCTCAGGACCCCTGGTCCGAGGTCCTCAGTATGGCTGCGTGGTGAATCTT
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Db	2821	GCCGGCCACGGGCTATTCCCTGTGTGGCGCTGCTGCTGGATACCCGACACCT
Qy	2888	GCAGAGCGACTACTCCAGCTATGCCCCGGACCTCCATCAGAGCGAGTCTCACCTTT
Db	2881	GCAGAGCGACTACTCCAGCTATGCCCCGGACCTCCATCAGAGCGAGTCTCACCTTT
Qy	2948	CGGCTTCAGGCTGGAGGAAATGCGTGCGRAACTCTTTGGGTGCTCTCGGGCT
Db	2941	CGGCTTCAGGCTGGAGGAAATGCGTGCGRAACTCTTTGGGTGCTCTCGGGCT
Qy	3008	TCACAGCCTGTTTCTCGAATTTGCAGGTGAACAGCTCCACAGCGGTGACACCAA
Db	3001	TCACAGCCTGTTTCTCGAATTTGCAGGTGAACAGCTCCACAGCGGTGACACCAA
Qy	3068	CAGATCTCTCTGCTGACGGCTACAGGTTTCACGCATGTGTGCTGACGCTCCCC
Db	3061	CAGATCTCTCTGCTGACGGCTACAGGTTTCACGCATGTGTGCTGACGCTCCCC
Qy	3128	TCAGCAAGTTTGAAAGAACCCACATTTTCTGCGCGTCACTCTGACACAGGCT
Db	3121	TCAGCAAGTTTGAAAGAACCCACATTTTCTGCGCGTCACTCTGACACAGGCT
Qy	3188	CTGCTACTCATCCTGAAAGCCAAAGACAGGATGTGCTGGGGGGCCAAAGGG
Db	3181	CTGCTACTCATCCTGAAAGCCAAAGACAGGATGTGCTGGGGGGCCAAAGGG
Qy	3248	CGGCGCTCTGCCCTCCGAGGCGTGCAGTGGCTGCCACCAAGACATTCCTGCT
Db	3241	CGGCGCTCTGCCCTCCGAGGCGTGCAGTGGCTGCCACCAAGACATTCCTGCT
Qy	3308	GACTCGACACCGTGTCACTTAAGTGGCACTCTCTGGGGTCACTCAGAGACGCCA
Db	3301	GACTCGACACCGTGTCACTTAAGTGGCACTCTCTGGGGTCACTCAGAGACGCCA
Qy	3368	GCTGAGTCGGAACTCCCGGGGACAGCTGACTGCCCTGGAGGCGCGACGCCAA
Db	3361	GCTGAGTCGGAACTCCCGGGGACAGCTGACTGCCCTGGAGGCGCGACGCCAA
Qy	3428	ACTGCCCTCAGACTTCAAGACCACTCTCGACTGATGGCCACCGCCCAACAGCA
Db	3421	ACTGCCCTCAGACTTCAAGACCACTCTCGACTGATGGCCACCGCCCAACAGCA
Qy	3488	GAGCAGACACAGAGCCCTGTCAAGCGCGGCTCTACGTCCAGGGAGGGAGGG
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secs

[illegible]

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Db	3181	CCTCCCTCTGTACTCCATCTCTGAAGCCACAGAACGAGGAGTGTGCGTGGGGGG
Qy	3241	GGCGCGCGGCGCCTCTGCGCCTCCGAGGCGGTGACGTGGCTGTGCCACCAAGCATTT
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Qy	3541	GGCGGCCCCACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCTTGAGTGAAGTGT
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Qy	3601	AGGCTTGCACTGTCGGGCTGAAGGCTGAGTGTCCGGCTGAGGCTCAGGCGTGAAGTGT
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Qy	3661	AAGGGTGTAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTC
Db	3661	AAGGGTGTAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTC
Qy	3721	CACCCACAGGGCCAGCTTTTTCCTCACAGGAGCCGGGCTTCCACTCCCCACATAGG
Db	3721	CACCCACAGGGCCAGCTTTTTCCTCACAGGAGCCGGGCTTCCACTCCCCACATAGG
Qy	3781	TCCATCCCAGATTGCCATTGTTTCAACCCCTCGCCCTGCGCCTCCTTTTGCCCTTCCA
Db	3781	TCCATCCCAGATTGCCATTGTTTCAACCCCTCGCCCTCCTTTTGCCCTTCCA
Qy	3841	ACCATCCAGGTGGAGACCTTGAGAGGACCTCTGGAGCTCTGGGAAATTGAGGTG
Db	3841	ACCATCCAGGTGGAGACCTTGAGAGGACCTCTGGAGCTCTGGGAAATTGAGGTG
Qy	3901	AGGTGTGCCCTGTACACAGGCGAGGACCTTGATCGACCTGGATGGGGGTCCCTGTGG
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Qy	3961	TTGGGGGGAGGTGCTGTGGGAGTAAATACTGAAATATATGAGTTTTTTCAGTTTTG
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Qy	4021	AAAAAAAAAAAAAAAAAAAAA 4042
Db	4021	AAAAAAAAAAAAAAAAAAAAA 4042

sequence encodes human telomerase reverse transcriptase which is a ribonucleoprotein. The present invention also includes the following methods: (A) determining whether a test compound is an inhibitor of hTERT, by detecting the change in hTERT recombinant polynucleotide, on administration of the compound; (B) determining whether a test compound is an activator of hTERT, by contacting a protein preparation of recombinant telomerase by contacting a protein preparation of recombinant RNA component; (C) detection of the hTERT RNA or protein in a sample by binding a relevant probe to the sample and detecting the complex formed or in the case of RNA detection, amplifying and correlating the presence of complex or amplification of the presence of hTERT in the sample; and (D) increasing the lifespan of a vertebrate cell by increasing hTERT expression; and (E) using an agent that causes an increase in cell vertebrate cell lifespan to create a medicament that inhibits ageing. A protein preparation of hTERT and the polynucleotide encoding hTERT can be used in the preparation of medicaments for inhibiting the effect of ageing or as inhibitors of telomerase activity can be used to treat conditions associated with high telomerase activity. A protein preparation of hTERT and the polynucleotide encoding hTERT can also be used in the new methods.

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 |||||
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 |||||
 CAGGAGACCAAGCTTTCAAAGAACAAGCTCTTTTCTTCTACCGCGGAGTCTCTGGAG 1808
 |||||
 GTTGTCAAGCAATTGGAATCAGACGACTTGAAGAGGGTGCAGCTGCGGAGCTGTC 1867
 |||||
 GTTGTCAAGCAATTGGAATCAGACGACTTGAAGAGGGTGCAGCTGCGGAGCTGTC 1868
 |||||
 AGCAGAGGTCAGGACAGCATCGGGAAGCAGCGCGCGCTCTGCTGACGTCAGACTCCG 1927
 |||||
 AGCAGAGGTCAGGACAGCATCGGGAAGCAGCGCGCGCTCTGCTGACGTCAGACTCCG 1928
 |||||
 CATCCCCAAGCCTGACGGGCTGCGGCCGATTTGTGAACATGGAATACTGCTCGTGGAGC 1987
 |||||
 CATCCCCAAGCCTGACGGGCTGCGGCCGATTTGTGAACATGGAATACTGCTCGTGGAGC 1988
 |||||
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 |||||
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 |||||
 CGTGCTCAACTACAGCGCGGCGCGCGCGCGCTCTCTGGGCGCTCTGTGCTGGG 2107
 |||||
 CGTGCTCAACTACAGCGCGGCGCGCGCGCGCTCTCTGGGCGCTCTGTGCTGGG 2108
 |||||

Qy	2108	CTTGAGCAGTATTCACAGGGCCTGGCGCACCTTCTGTCTGTCGTGTGGGGCCCA
Db	2101	CTTGAGCAGTATTCACAGGGCCTGGCGCACCTTCTGTCTGTCGTGTGGGGCCCA
Qy	2168	GC CGCCTGAGCTGTACTTTTGTCAAGTTCGATGTGACGGGCGCGTACGACACCAT
Db	2161	GC CGCCTGAGCTGTACTTTTGTCAAGTTCGATGTGACGGGCGCGTACGACACCAT
Qy	2228	GGACAGGCTCACGGAGGTTCATCGCCAGCATCATCAAAACCCAGAACACGTACTGC
Db	2221	GGACAGGCTCACGGAGGTTCATCGCCAGCATCATCAAAACCCAGAACACGTACTGC
Qy	2288	TCGGTATGCCGTGTGTCAGAGAGCGCGCCATGGGCACTCGCAAGCGCTTCAC
Db	2281	TCGGTATGCCGTGTGTCAGAGAGCGCGCCATGGGCACTCGCGCAAGCGCTTCAC
Qy	2348	CGTCTCTACTTGA CAGACCTCCAGCCGTACATCGCAGAGTTCGTGGCTCACCTC
Db	2341	CGTCTCTACTTGA CAGACCTCCAGCCGTACATCGCAGAGTTCGTGGCTCACCTC
Qy	2408	GACCAAGCCCGCTGAGGGATGCCGTCTCATCGAGCAGAGCTCTCCCTCGAATGAC
Db	2401	GACCAAGCCCGCTGAGGGATGCCGTCTCATCGAGCAGAGCTCTCCCTCGAATGAC
Qy	2468	CAGTGGCCTCTTCGACGCTCTTCCTACGCTTCATGTGCCACACGCCGTGGCATC
Db	2461	CAGTGGCCTCTTCGACGCTCTTCCTACGCTTCATGTGCCACACGCCGTGGCATC
Qy	2528	CAAGTCTACGTCAGTCGCGAGGGGATCCCGAGGGCTCCATCTCTCTCAAGCTC
Db	2521	CAAGTCTACGTCAGTCGCGAGGGGATCCCGAGGGCTCCATCTCTCTCAAGCTC
Qy	2588	CAGCCTGTGTACTCGCGCAGCATGGAGAACAGACTGTTTGGGGGATTCGGCGGAC
Db	2581	CAGCCTGTGTACTCGCGCAGCATGGAGAACAGACTGTTTGGGGGATTCGGCGGAC
Qy	2648	GCTCTCGCTTGTGGTGGAGATTTCTTGTGGTGACACCTCACTCAACCCACGCG
Db	2641	GCTCTCGCTTGTGGTGGAGATTTCTTGTGGTGACACCTCACTCAACCCACGCG
Qy	2708	CTTCTCTCAGGACCTGTGTCGAGGTGTCCTTGAGTATGGCTGTGCTGTGAACTTG
Db	2701	CTTCTCTCAGGACCTGTGTCGAGGTGTCCTTGAGTATGGCTGTGCTGTGAACTTG
Qy	2768	GACAGTGGTGAATTCCTCTGTAGAAGACGAGGCCCTGGGTGGCGACGGCTTTGT
Db	2761	GACAGTGGTGAATTCCTCTGTAGAAGACGAGGCCCTGGGTGGCGACGGCTTTGT
Qy	2828	GCCGCGCCACCGCCTATTCCTCTGGTGGGCGCTGCTCTGGATACCGCGACCTTG
Db	2821	GCCGCGCCACCGCCTATTCCTCTGGTGGGCGCTGCTCTGGATACCGCGACCTTG
Qy	2888	CGAGAGCGACTACTCCAGCTATGCCGGACCTCCATCAGAGCCAGTCTCACCTTC
Db	2881	CGAGAGCGACTACTCCAGCTATGCCGGACCTCCATCAGAGCCAGTCTCACCTTC
Qy	2948	CGGCTTCAAGGCTGGGAGGAACATCGCTCGCAAACTCTTTGGGGCTTTGGGGCTG
Db	2941	CGGCTTCAAGGCTGGGAGGAACATCGCTCGCAAACTCTTTGGGGCTTTGGGGCTG
Qy	3008	TCACAGCCTGTTTCTGGATTTGCAAGGTGAACAGCCTCCAGACGGTGTGACCAAC
Db	3001	TCACAGCCTGTTTCTGGATTTGCAAGGTGAACAGCCTCCAGACGGTGTGACCAAC
Qy	3068	CAAGATCCTCTGCTGACGGGTA CAGGTTTACGGATGTGTGCTGTGAGCTTCCA
Db	3061	CAAGATCCTCTGCTGACGGGTA CAGGTTTTCACGATGTGTGCTGTGAGCTTCCA
Qy	3128	TCAGACAAGTTTGGAGAACCCCAATTTTTTCTGGCGGTATCTCTGACACGGCC
Db	3121	TCAGACAAGTTTGGAGAACCCCAATTTTTTCTGGCGGTATCTCTGACACGGCC
Qy	3188	CTGTACTCTCCATCTCGAAGAGCAGAGAACCGCAGGGATGTCTGGGGGGCCAAAGGG

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3CAGACACCAAGAGCCCTGTACGCCGGGCTTACGTCCAGGGAGGAGGGCGGCC 3540
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|||||
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|||||
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|||||
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|||||
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|||||
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|||||
3GATTCGCCATTTTTCACCCCTCGCCCTGCGCTTTCCTTTCCTTCCACCCCGCCATCC 3840
|||||
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|||||
3TGGAGACCTTGAGAGGACCCCTGGAGTCTGGGAATTTGGAGTACCAAAAGTGTG 3900
|||||
3TGTACACAGGCGAGACCCCTGCACCTGGATGGGCTCCCTGTGGTCAAAATGGGG 3967
|||||
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|||||
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|||||
3GTGCTGGGAGTAAATACTGAATATATGAGTTTTTTCAGTTTTTGAATAAAAAA 4020
|||||
3AAAAAAAAAAAA 4042
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3AAAAAAAAAAAA 4035

```

undard; cDNA; 4023 BP.

(first entry)

rase gene referred to as hEST2.

bunit; human; telomerase; telomere maintenance; diagnosis; cancer; ss.

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OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 59..3458
XX /*tag= a
PN WO9837181-A2.
XX
PD 27-AUG-1998.
XX
PF 20-FEB-1998; 98WO-US003404.
XX
PR 20-FEB-1997; 97US-0038750P.
PR 20-MAY-1997; 97US-0047151P.
PR 01-AUG-1997; 97US-0054549P.
PR 14-AUG-1997; 97US-0055762P.
PR 30-OCT-1997; 97US-0064322P.
XX
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
Counter CM, Meyerson M, Weinberg RA;
XX
WPI; 1998-495367/42.
XX P-PSDB; AAW71376.
XX
PT New isolated human telomerase catalytic sub-unit gene - used to
PT products for increasing or reducing the life span of cells such
PT cells or transformed cells.
XX
PS Claim 5; Fig 5A-B; 96pp; English.
XX
CC The present sequence encodes the catalytic subunit of a human t
CC holoenzyme. Disruption of the telomerase gene alters telomere
CC maintenance. The DNA is essential for telomerase activity, and t
CC protein is physically associated with telomerase and a constitut
CC active telomerase complex. The products can be used for increas
CC reducing the lifespan of cells such as cancer cells or transfor
CC They can also be used in the diagnosis and treatment of maligna
CC addition, cells with a longer lifespan can be transplanted into
CC grafted onto an individual (e.g. as skin grafts, as systems for
CC of therapeutic proteins, such as hormones and enzymes), to whom
CC provide therapeutic benefit
XX
SQ Sequence 4023 BP; 668 A; 1363 C; 1277 G; 715 T; 0 U; 0 Other;
Query Match 99.5%; Score 4019.8; DB 2; Length 4023;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4021; Conservative 0; Mismatches 2; Indels 0;
Qy 5 CAGGACGCGTGGTCTGCTGGCGCAGTGGGAGCCCTGGCCCGGCCACCCCG
Db 1 CAGGACGCGTGGTCTGCTGGCGCAGTGGGAGCCCTGGCCCGGCCACCCCG
Qy 65 GCGCGCGCTCCCGCTGCGGAGCGGTGCGCTCCCTGCTGCGAGCCACTACCG
Db 61 GCGCGCGCTCCCGCTGCGGAGCGGTGCGCTCCCTGCTGCGAGCCACTACCG
Qy 125 GCTGCGCGTGGCCACGTTGCTGGGGCGCTGGGGCCCCAGGGCTGGCGGTGGT
Db 121 GCTGCGCGTGGCCACGTTGCTGGGGCGCTGGGGCCCCAGGGCTGGCGGTGGT
Qy 185 CGGGGACCCCGCGGCTTTCCGCGCGCTGGTGGGCCAGTGGCTGGCTGGCC
Db 181 CGGGGACCCCGCGGCTTTCCGCGCGCTGGTGGGCCAGTGGCTGGCTGGCC
Qy 245 CGACGCGCGCCCGCCCGCCCGCCCTTCCTTCGCCAGGTGCTTCGCTGAAGAG
Db 241 CGACGCGCGCCCGCCCGCCCGCCCTTCCTTCGCCAGGTGCTTCGCTGAAGAG
Qy 305 GCGCGCGAGTCTCAGAGGCTGTGCGGAGCGCGCGGAGAAAGTGTGGCTTC
Db 301 GCGCGCGAGTCTCAGAGGCTGTGCGGAGCGCGCGGAGAAAGTGTGGCTTC

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3CAAGTCCTACGTCAGCTGCCAGGGGATCCCGCAGGGCTCCATCTCTTCCACGCGTCT 2580

3CAGCCTGTGCTACGGCGACATGGAGAACAAAGCTGTTTGGGGGATTCGGCGGACGG 2644

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IGCTCCTCGCGTTGGTGGATGATTTCTGTGTGGTGAACCTCACCTCACCCACGGGAA 2700

CCTTCTCAGGACCCCTGCTCCGAGGTGTCCCTCAGTATGGCTGCGTGGTGAACCTTGGC 2764

CCTTCTCAGGACCCCTGCTCCGAGGTGTCCCTCAGTATGGCTGCGTGGTGAACCTTGGC 2760

AGACAGTGGTGAATCCCTGTGAGAGACAGAGCCCTGGTGGGACAGCGCTTTGTTC 2824

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3TCACAGCTGTTTCTGATTTTCAGGTGAACAGCCTCCAGACGGTGTGCACCAACAT 3060

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ACAGATCCTCCTGCTGCGGGGTACAGGTTTACGCAATGTGTGCTGAGTCCCATTT 3120

ATCAGCAAGTTTGGAGAAACCCACATTTTCTCGCGCTCATCTGCACAGCGGCTC 3184

ATCAGCAAGTTTGGAGAAACCCACATTTTCTCGCGCTCATCTGCACAGCGGCTC 3180

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CTGTCTACTCATCTTGAAGCAAGAACGAGGAGATGTGCTGGGGGCAAGGGCGC 3240

CGCGCCCTCTGCCCCTCCGAGGCCGTGACGTGGCTGTGCCACCAAGCATTTCTGTCTCAA 3304

CGCGCCCTCTGCCCCTCCGAGGCCGTGACGTGGCTGTGCCACCAAGCATTTCTGTCTCAA 3300

GACTCGAACACCGTGTCACTACGTGCCACTCCTGGGCTACTCGGAGCAGCCCGAGC 3364

GACTCGAACACCGTGTCACTACGTGCCACTCCTGGGCTACTCGGAGCAGCCCGAGC 3360

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ACTGCCCTCAGACTTCAAGACCATCCTGGACTGTATGGCCACCCGCCCAAGCCAGGC 3480

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CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCTGAGTGGTGGTGGTGGTGGTGG 3600

CATGTCCGGCTGAAGGCTGAGTGTCCGGCTCAGGCTTGAAGGCTGTGAGTGGTGGTGG 3664

CATGTCCGGCTGAAGGCTGAGTGTCCGGCTCAGGCTTGAAGGCTGTGAGTGGTGGTGG 3660

Qy	3665	GCTGAGTGTCACGACACACCTGGCGTTCTTCACTTCCCCACAGAGCTGGCGCTCGGG	
Db	3661	GCTGAGTGTCACGACACACCTGGCGTTCTTCACTTCCCCACAGAGCTGGCGCTCGGG	
Qy	3725	CCAGGGCCAGCTTTTCCCTCACAGGAGCCGGCTTCCACTCCCCACATAGGAAT	
Db	3721	CCAGGGCCAGCTTTTCCCTCACAGGAGCCGGCTTCCACTCCCCACATAGGAAT	
Qy	3785	TCCCCAGATTGCGCAATTGTTCAACCCTCGCCCTGCGCTCCTTTGCTTCCACCC	
Db	3781	TCCCCAGATTGCGCAATTGTTCAACCCTCGCCCTGCGCTCCTTTGCTTCCACCC	
Qy	3845	TCCAGGTGGAGACCTTGAGAGGACCTGGGAGCTCTGGAAATTTGGAGTGACCC	
Db	3841	TCCAGGTGGAGACCTTGAGAGGACCTGGGAGCTCTGGAAATTTGGAGTGACCC	
Qy	3905	GTCCCTGTACACAGGCGAGGACCTGCACTGGATGGGGGTCCCTGTGGGGTCA	
Db	3901	GTCCCTGTACACAGGCGAGGACCTGCACTGGATGGGGGTCCCTGTGGGGTCA	
Qy	3965	GGGGAGGTGCTGTGGGAGTAAATACTGTAATATATAGAGTTTTTCAGTTTTTGAAA	
Db	3961	GGGGAGGTGCTGTGGGAGTAAATACTGTAATATATAGAGTTTTTCAGTTTTTGAAA	
Qy	4025	AAA 4027	
Db	4021	AAA 4023	

RESULT 4

ABL53711	
ID	ABL53711 standard; cDNA; 4070 BP.
XX	
XX	AC
XX	ABL53711;
XX	
DT	17-JUN-2002 (first entry)
XX	
DE	Human telomerase catalytic subunit hTERT cDNA.
XX	
KW	hTERT; telomerase; reverse transcriptase; immortalisation; human vaccine; enzyme; gene; ss.
KW	
OS	Homo sapiens.
XX	
PN	WO200216555-A2.
XX	
PD	28-FEB-2002.
XX	
Pf	17-AUG-2001; 2001WO-GB003726.
XX	
PR	17-AUG-2000; 2000GB-00020246.
PR	17-AUG-2000; 2000US-0225734P.
XX	
PA	(UYWA-) UNIV WALES COLLEGE OF MEDICINE.
XX	
PI	Jones CJ, Kipling DG, Wilkinson G, Mcharry B, Skinner JW;
XX	
DR	WPI; 2002-315462/35.
XX	
PT	Novel hTERT-immortalized cell line (human telomerase reverse transcriptase) useful for human vaccine production and preparati
PT	antigen, such as a virus or virus-derived agent.
PS	Example 1; Fig 1; 64pp; English.

The present sequence is that of hTERT cDNA in plasmid pGRN121.1. The catalytic subunit of human telomerase. Claimed immortalised cell lines for use in vaccine production are adapted to express hTERT. Suitable cell lines comprise human diploid fibroblasts, e.g. WRc WI38 cells, transfected with hTERT cDNA or infected by a retrovirus carrying hTERT cDNA, and are capable of supporting antigen production for preparing such cell lines using recombinant antigen production method for preparing such cell lines using recombinant techniques.

The cell lines are also used as a diagnostic test for the virus, such as human cytomegalovirus, and to determine the antiviral agents by testing the capability of a modified reporter gene to infect the cells. The cell lines have which can be impaired in cell lines immortalised by other being able to support viral replication. The cells remain fully suitable for viral/vaccine cultivation

70 BP; 670 A; 1383 C; 1296 G; 721 T; 0 U; 0 Other;

99.3%; Score 4015.4; DB 6; Length 4070;

Accuracy 100.0%, Freq. NO. 0;
Conservative 0; Mismatches 1; Indels 0; Gaps 0;

!CAGCGCTGGCTCTGCTGGCACGTGGGAAGCCCTGGCCCCCGGCCACCCCCGGCATG 65

!CAGCGCTGCGTCCTGTCTGCGCACGTGGGAAGCCCTGGCCCCGGGCCACCCCCGGGATG 78

!CGCGCTCCCGCTGCCGAGCGGTGGCTCCCTGCTGCGAGCCACTACCGCGAGGTG 125

CGGGCTCCCGGCTGCCGAGCCGTGGCTCCCTGCTGCGCAGCCACTACCGCAGGTG 138

!CGCTGCCACGTTCTGTGGGGCCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGGCG 185

!CGCTGGCCACGTTCTGTGGGGCGCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGGGC 198

!GACCCGGGGGCTTTCCGGCGCGCTGGTGGCCCACTGCCCTGGTGTGGTGGCCCTGGAC 245

'GACCCGGCGGCTTTCCGCGCGCTGGTGGCCCA GTCCCTGGTGCGGTGCCCTGGGAC' 258

CGGGCGCCCCCGGGCCCCCTCTCGGCCAGGTGTCCTGCTGTGAAGGAGCTCATC

CGCGCGCCCCCGCGCCCCCTCTCCGCCAGGTGTCTGCGCTGAAGAGCTGGTG 318

'CGAGTGTCTGCAGAGGCTGTGCCAGCGCGCGGCGAAGACGTCGTGGCTTCCGCTTC 355

CGAGTGTGCAGAGGCTGTCCGAGCGCGCGCGCAAGAACTGTCTGGCTTCCGCTTC 378

CTGCTGGA CCGGGCCCGGGGGCCCCCGAGCCCTTCA CCAACAGCGCTCCGACG

CTGGTGGACGGGGGCGGGGGGGCCCCCGCCGCTTTTCACCAAGCAGGCCAACCA

CCTGCCCCACACCGCCGACCCAGCCCACCTGGCCTCCATCCGTCCTCCTTCTGCTG

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CONCLUSIONS

[illegible][illegible][illegible][illegible][illegible][illegible]

CGTGGACCGGAGGACCGGGTTCCTGCTGGTGTCACCTGGCAGACCCGCGGAAGAA 905

CGTGGGACCGAGTGGCCGAGACCTCCGCCGGAAGAA 918

Qy	906	GCACCTCTTTGGAGGGTGGCTCTCTCTGGACGCGCCACTCTCGGACGCGCCACTCTCGGACGCGGCCACTCCACCCCAATCCCGTGT
Db	919	GCCACTCTTTTGGAGGGTGGCTCTCTCTGGACGCGGCCACTCCACCCCAATCCCGTGT
Qy	966	CAGCACACGCGGGCCCCCATCTCCATCGCGGCCACACGCTCCCTGGGACACG
Db	979	CAGCACACGCGGGCCCCCATCTCCATCGCGGCCACACGCTCCCTGGGACACG
Qy	1026	CCCCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCTCAGGCGGACAAGGAG
Db	1039	CCCCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCTCAGGCGGACAAGGAG
Qy	1086	CGCGCTCTCTTCTACTCTCAGCTCTCTGAGGCCCGACCTGACTGCGGCTCTCGAGG
Db	1099	CGCGCTCTCTTCTACTCTCAGCTCTCTGAGGCCCGACCTGACTGCGGCTCTCGAGG
Qy	1146	GAGACCATCTTTCTGGGTTTCCAGGCCCCGATGCGAGGACATCTCCCGCAGGTTGT
Db	1159	GAGACCATCTTTCTGGGTTTCCAGGCCCCGATGCGAGGACATCTCCCGCAGGTTGT
Qy	1206	CTGCGCCAGCGCTACTTGGCAAAATGCGGCCCTGTCTTCTGAGAGCTGCTTTGGGAAAC
Db	1219	CTGCGCCAGCGCTACTTGGCAAAATGCGGCCCTGTCTTCTGAGAGCTGCTTTGGGAAAC
Qy	1266	CAGTGCCCTTACGGGCTGCTCTCTCAGAGCGCACTGCCCGCTCGCAGCTCGCGTCT
Db	1279	CAGTGCCCTTACGGGCTGCTCTCTCAGAGCGCACTGCCCGCTCGCAGCTCGCGTCT
Qy	1326	GCAGCGGTGTCTGTGCCCGGAGAGCCCAAGGCTCTGTGGCGGCCCCCGAG
Db	1339	GCAGCGGTGTCTGTGCCCGGAGAGCCCAAGGCTCTGTGGCGGCCCCCGAG
Qy	1386	GACACAGACCCCGTCGCTGTGCGAGCTGCTCGCGCAGACACAGCAGCGCCCTGG
Db	1399	GACACAGACCCCGTCGCTGTGCGAGCTGCTCGCGCAGACACAGCAGCGCCCTGG
Qy	1446	TACGGCTTCTGTGGGCTTGCCTCGCGCGGCTGTGTGCCCGCAGGCTCTGTGGCGCTCTGGGCT
Db	1459	TACGGCTTCTGTGGGCTTGCCTCGCGCGGCTGTGTGCCCGCAGGCTCTGTGGGCT
Qy	1506	CACAAAGAACGCGCTTCTCTCAGGAACACCAAGAGTTTCATCTCCCTGGGGAAG
Db	1519	CACAAAGAACGCGCTTCTCTCAGGAACACCAAGAGTTTCATCTCCCTGGGGAAG
Qy	1566	AAGCTCTCGCTGCAGGAGCTGACGTGGAGAGATGAGCGTGGGACCTGCGCTTGG
Db	1579	AAGCTCTCGCTGCAGGAGCTGACGTGGAGAGATGAGCGTGGGACCTGCGCTTGG
Qy	1626	AGAGGCCACAGGGTGTGTGTGTTTCCGCGCGCAGACACCGTCTCGCTGAGGAG
Db	1639	AGAGGCCACAGGGTGTGTGTGTTTCCGCGCGCAGACACCGTCTCGCTGAGGAG
Qy	1686	GCCAAGTCTCTCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGCTCT
Db	1699	GCCAAGTCTCTCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGCTCT
Qy	1746	TATGTACAGGACCAACGCTTTCAAAGAACAGGCTCTTTTTTACCGGAAAGTGT
Db	1759	TATGTACAGGACCAACGCTTTCAAAGAACAGGCTCTTTTTTACCGGAAAGTGT
Qy	1806	AGCAAGTTGCAAGCATTTGGATCAGACAGCACTTGAAGAGGTGACAGTGGCGG
Db	1819	AGCAAGTTGCAAGCATTTGGATCAGACAGCACTTGAAGAGGTGACAGTGGCGG
Qy	1866	TGGAGACAGAGGTACGCGACCATCGGGAAGCCAGGCCCCGCCCTGTGAGCTCA
Db	1879	TGGAGACAGAGGTACGCGACCATCGGGAAGCCAGGCCCCGCCCTGTGAGCTCA
Qy	1926	CGCTTCATCCCAAGCCTGACGGGCTCGGCCGATTTGTGAACATGGAATACGTCG
Db	1939	CGCTTCATCCCAAGCCTGACGGGCTCGGCCGATTTGTGAACATGGAATACGTCG

TCTCGCTGCGAGAGCTGACGTGGGAAGATGAGCGTGGCGGACTCGCTTGGCTGGCGCAG	1637
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TCA CGGAGACCAACGTCTTCAAAGAAACAGGCTCTTTTCTTACCGGAAGAGTGTCTGGAG	1807
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CGCTGCTCAACTACGAGCGGGCGCGCGCCCGCCCTCTGCTGGGCGCTCTGTGCTGGG	2100
TGGACGATATCCACAGGGCCCTGGCGCACCTTCTGTGCTGCGTGTGGGGCCACGAGACCC	2167
TGGACGATATCCACAGGGCCCTGGCGCACCTTCTGTGCTGCGTGTGGGGCCACGAGACCC	2160
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GGTATGCGGTGGTCCAGAAAGGCCGCCCATGGGCACGTTCGCAAGGCCCTTCAAGAGCCA	2340
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QY	2648	GCTCTCTGCGTTTGGTGGATGATTTCTTTGTTGGTGACACCTCACCTCACCCACCG
DB	2641	GCTCTCTGCGTTTGGTGGATGATTTCTTTGTTGGTGACACCTCACCTCACCCACCG
QY	2708	CTTCTCTCAGGACCCCTGGTCCGAGGTGTCCCTTGAGTATGGCTGGGTGGTGAACCTT
DB	2701	CTTCTCTCAGGACCCCTGGTCCGAGGTGTCCCTTGAGTATGGCTGGGTGGTGAACCTT
QY	2768	GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGGTGGCACCGCTTTTGTG
DB	2761	GACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGGTGGCACCGCTTTTGTG
QY	2828	GCCGGCCCCACGGCCCTATATCCCTCTGGTGGCCCTGCTCTGGATACCCGGACCCCT
DB	2821	GCCGGCCCCACGGCCCTATATCCCTCTGGTGGCCCTGCTCTGGATACCCGGACCCCT
QY	2888	GCAGAGCGACTACTTCAGCTATATGCCCGGACCTTCATCAGAGCCAGTCTCACCTT
DB	2881	GCAGAGCGACTACTTCAGCTATATGCCCGGACCTTCATCAGAGCCAGTCTCACCTT
QY	2948	CGGCTTCAAGGCTGGGAGGAACATGCGTCGCCAAACTCTTTTGGGGTCTTCGGGCT
DB	2941	CGGCTTCAAGGCTGGGAGGAACATGCGTCGCCAAACTCTTTTGGGGTCTTCGGGCT
QY	3008	TCA CAGGCTGTCTTCGTATTTG CAGGTGAA CAGCCTCCAGACGGTGTGACCAAA
DB	3001	TCACAGGCTGTCTTCGTATTTG CAGGTGAA CAGCCTCCAGACGGTGTGACCAAA
QY	3068	CAAGATCCTCTGCTGCAGGCGTACAGTTT CAGCATGTGTGTCTG CAGCTCCC
DB	3061	CAAGATCCTCTGCTGCAGGCGTACAGTTT CAGCATGTGTGTCTG CAGCTCCC
QY	3128	TCAGCAAGTTTGGAAAGAACCCACATTTTTCTGCGCGTCATCTCTGACACGGC
DB	3121	TCAGCAAGTTTGGAAAGAACCCACATTTTTCTGCGCGTCATCTCTGACACGGC
QY	3188	CTGCTACTCCATCTCTGAAAGCCAGAACACAGGGATGTGCTGGGGGCCAAGGG
DB	3181	CTGCTACTCCATCTCTGAAAGCCAGAACACAGGGATGTGCTGGGGGCCAAGGG
QY	3248	CGGGCCTCTGGCCTCCGAGGCCGTG CAGTGCGTGTGTGCCACCAAGCATTCCTGCT
DB	3241	CGGGCCTCTGGCCTCCGAGGCCGTG CAGTGCGTGTGTGCCACCAAGCATTCCTGCT
QY	3308	GACTCGACACCGTGTCACTTGA GTGTCACCTCTCTGGGTCACTTCAGACAGCCCA
DB	3301	GACTCGACACCGTGTCACTTGA GTGTCACCTCTCTGGGTCACTTCAGACAGCCCA
QY	3368	GCTGAGTCGGAAGCTCCCGGGACGACGCTGACTGCCCTGGAGGGCCGAGCCAA
DB	3361	GCTGAGTCGGAAGCTCCCGGGACGACGCTGACTGCCCTGGAGGGCCGAGCCAA
QY	3428	ACTGGCCTCAGACTTCAAGACCATCTTGACATGTATGGCCACCCGCCACAGCCA
DB	3421	ACTGGCCTCAGACTTCAAGACCATCTTGACATGTATGGCCACCCGCCACAGCCA
QY	3488	GAGCAGACACCAAGCAGCCTGT CAGCGGGCTCTACGTCGCCAGGAGGGAGGG
DB	3481	GAGCAGACACCAAGCAGCCTGT CAGCGGGCTCTACGTCGCCAGGAGGGAGGG
QY	3548	CACACCCAGCCCGCACCGCTGGGAGTCTGAGGCGCTGAGTGTTTTGGCCGAG
DB	3541	CACACCCAGCCCGCACCGCTGGGAGTCTGAGGCGCTGAGTGTTTTGGCCGAG
QY	3608	CATGTCCGGCTGAAGGCTGAGTGT CGGGCTGAGGCGCTGAGCGAGTGTCCAGCCAF
DB	3601	CATGTCCGGCTGAAGGCTGAGTGT CGGGCTGAGGCGCTGAGCGAGTGTCCAGCCAF
QY	3668	GAGTGTCCAGCACACCTGGCGCTTTTCACTTCCCCACAGCGCTGGCGCTCGGCTCG
DB	3661	GAGTGTCCAGCACACCTGGCGCTTTTCACTTCCCCACAGCGCTGGCGCTCGGCTCG
QY	3728	GGGCCAGGCTTTTCTCTCAC CAGAGAGCCCGGCTTTCAC TCCCCACATAGGAA TAGT

[illegible]

standard; cDNA; 4015 BP.

(first entry)

reverse transcriptase (hTRT) cDNA.

reverse transcriptase; human; hTERT; cell proliferation;

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Location/Qualifiers
56. .3454
/*tag= a
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99WO-US007097.

98US-00052864.

98US-00128354.

IN CORP.

0842/52.
2090.

c polypeptide and polynucleotide, useful for increasing tivity in a cell.

Fig 2; 24pp; English.

nucleotide sequence of cDNA encoding human telomerase reverse transcriptase (hTERT, see AAY32090). Human telomerase is a target for many anti-neoplastic drugs and treating diseases relating to cell proliferation and differentiation, such as cancer, or for increasing the proliferative capacity of stem cells. A claimed method for increasing the proliferative capacity of a cell, especially a human or other mammalian cell, involves introducing into the cell a recombinant hTERT polynucleotide encoding an hTERT protein having amino acid residues 192-323, 192-271, 200-271, 222-271, 192-323 and 415-450, or 192-271 and 415-450 are deleted. A method for reducing telomerase activity in a cell involves introducing into the cell a recombinant polynucleotide encoding an hTERT variant having amino acids 192-450, 560-565, 637-660, 638-660, 748-764 or 765-764. The hTERT polynucleotides are obtained by mutagenesis of the hTERT gene.

CC	coding sequence
XX	
SQ	Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
	Query Match 99.3%; Score 4015; DB 2; Length 4015;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 4015; Conservative 0; Mismatches 0; Indels 0;
QY	8 GCAGCGCTGCGTCTCTGCTGCGCACGTGTGGAAAGCCCTGGCCCCCGCGCCACCCCCGCG
DB	1 GCAGCGCTGCGTCTCTGCTGCGCACGTGTGGAAAGCCCTGGCCCCCGCGCCACCCCCGCG
QY	68 GCGCGCTCCCGCTGCCGAGCGGTGCGCTCCCTGCTGCGCAGCCACTACGCGCA
DB	61 GCGCGCTCCCGCTGCCGAGCGGTGCGCTCCCTGCTGCGCAGCCACTACGCGCA
QY	128 GCGCTGTGGCCAGCTTCTGTCGCGCGCTGGGGCCCCAGGGCTGGCGGCTGTGTGCA
DB	121 GCGCTGTGGCCAGCTTCTGTCGCGCGCTGGGGCCCCAGGGCTGGCGGCTGTGTGCA
QY	188 GGACCCGCGCGGCTTTCCGCGCGGCTGGTGGCCCCAGTGCCTGGTGTGGCTGCCCTG
DB	181 GGACCCGCGCGGCTTTCCGCGCGGCTGGTGGCCCCAGTGCCTGGTGTGGCTGCCCTG
QY	248 ACGGGCGGCCCGCGCGGCCCTCTCTTCCGCGCAGGTGTCTGTCTGAAGAGCT
DB	241 ACGGGCGGCCCGCGCGGCCCTCTCTTCCGCGCAGGTGTCTGTCTGAAGAGCT
QY	308 CCGAGTGTGCAGAGGCTGTGCGAGCGGGCGCGGAAGACGTGCTGGCGCTTCGG
DB	301 CCGAGTGTGCAGAGGCTGTGCGAGCGGGCGCGGAAGACGTGCTGGCGCTTCGG
QY	368 GCTGCTGGAACGCGGGCCCGCGGGGGCCCCCGAGGCCCTTACACACAGCGCTGGCG
DB	361 GCTGCTGGAACGCGGGCCCGCGGGGGCCCCCGAGGCCCTTACACACAGCGTGGCG
QY	428 CTTGCCCAACACGCTGTACCGACGCACTGTCCGGGGAGCGGGCGTGTGGGGCTGTCT
DB	421 CTTGCCCAACACGCTGTACCGACGCACTGTCCGGGGAGCGGGCGTGTGGGGCTGTCT
QY	488 CCGCGTGGGGCGACGACGTGTGGTGTCACTGTGGCAAGTGTGGCGCTCTTTGT
DB	481 CCGCGTGGGGCGACGACGTGTGGTGTCACTGTGGCAAGTGTGGCGCTCTTTGT
QY	548 GGCTCCCAAGCTGCGCTACCAAGTGTGCGGGCCCGCGCTGTACCAAGCTCCGCGCT
DB	541 GGCTCCCAAGCTGCGCTACCAAGTGTGCGGGCCCGCGCTGTACCAAGCTCCGCGCT
QY	608 TCAGCGCCCGGCCCGCGCACAGCTAGTGTGAACCCGAAGGCGTGTGGGATGCGAJ
DB	601 TCAGCGCCCGGCCCGCGCACAGCTAGTGTGAACCCGAAGGCGTGTGGGATGCGAJ
QY	668 CTTGGAACCATAGCTCAGGGAGCGGGGTTCCCTCTGGGCTGTGCAGCCCCGGGG
DB	661 CTTGGAACCATAGCTCAGGGAGCGGGGTTCCCTCTGGGCTGTGCAGCCCCGGGG
QY	728 GAGGCGCGGGGGCAGTGTGCACGCAAGTCTGCGGTTGCCCAAGAGGCCACAGGCGT
DB	721 GAGGCGCGGGGGCAGTGTGCACGCAAGTCTGCGGTTGCCCAAGAGGCCACAGGCGT
QY	788 TGCCCCCTGAGCCGAGCGGACGCCGCTTGGGCGAGGGGTCTCTGGGCCCCACCGCGG
DB	781 TGCCCCCTGAGCCGAGCGGACGCCGCTTGGGCGAGGGGTCTCTGGGCCCCACCGCGG
QY	848 GCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACTGTGCAGACCCGCGGAP
DB	841 GCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACTGTGCAGACCCGCGGAP
QY	908 CACTCTTTGGAGGGTGGCTCTCTGGCAACGCGCACTCCCAACCCATCCGTGGGG
DB	901 CACTCTTTGGAGGGTGGCTCTCTGGCAACGCGCACTCCCAACCCATCCGTGGGG
QY	968 GCACGACGGCGGGCCCCCATCCACATCGCGGGCCACCAAGTCCCGGGGACACGCGCT

standard; cDNA; 4015 BP.

ing a human telomerase reverse transcriptase (TRT).

reverse transcriptase; TRT; T lymphocyte activation;
cell; telomerase activity; cancer cell; proliferating cell;
cell destruction; telomerase; cancer; proliferation disease; ss.
).

XX	Key	Location/Qualifiers	
FH	CDS	56...3454	
FT		/*tag= a	
FT		/product= "telomerase reverse transcriptase"	
XX			
XX	W09950392-A1.		
XX			
PD	07-OCT-1999.		
XX			
PF	30-MAR-1999;	99WO-US006898.	
XX			
PR	31-MAR-1998;	98US-0112006P.	
XX			
PA	(GERO-) GERON CORP.		
XX			
PI	Gaeta FCA;		
XX			
DR	WFI; 1999-610845/52.		
DR	P-PSDB; AAY43621.		
XX			
PT	Elliciting an in vivo immune response for prevention and treatme		
PT	cancers.		
XX			
PS	Disclosure; Fig 2; 26pp; English.		
XX			
CC	The present sequence encodes a human telomerase reverse transcriptase (TRT) polypeptide. The protein is used in the method of the invention for activating a T lymphocyte with a dendritic cell th		
CC	comprising contacting the T lymphocyte with a dendritic cell th		
CC	expresses a TRT peptide in the context of a MHC class I or MHC		
CC	molecule. The protein causes induction of an in vivo immunologi		
CC	response to telomerase activity. Cancer cells are characterized		
CC	expression of endogenous TRT gene and the presence of detectabl		
CC	telomerase activity. Therefore, by eliciting a specific immune		
CC	to TRT or to TRT-expressing cells, it is possible to selectivel		
CC	proliferating cells for immunological destruction. The method i		
CC	eliciting an in vivo immune response to telomerase by activati		
CC	lymphocyte, and is useful for prevention and treatment of cance		
CC	other proliferation diseases/conditions		
XX			
SQ	Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;		
Query Match 99.3%; Score 4015; DB 2; Length 4015;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 4015; Conservative 0; Mismatches 0; Indels 0;			
QY	8	GCAGCGCTGCGTCTGCTGCGCAGCTGTGGAGAGCCCTGGCCCCCGGCCACCCCGCG	
DB	1	GCAGCGCTGCGTCTGCTGCGCAGCTGTGGAGAGCCCTGGCCCCCGGCCACCCCGCG	
QY	68	GCGCGCTCCCGCTGCCGAGCCGTGCGCTCCCTGCTGGCAGCCACTACCGCGA	
DB	61	GCGCGCTCCCGCTGCCGAGCCGTGCGCTCCCTGCTGGCAGCCACTACCGCGA	
QY	128	GCGCTGCGCCACGTTGCTGCGCGCGCTGGGGCCCCCAGGGCTGGCGGTGGTGCA	
DB	121	GCGCTGCGCCACGTTGCTGCGCGCGCTGGGGCCCCCAGGGCTGGCGGTGGTGCA	
QY	188	GAACCCCGCGGCTTTCCGCGCGCTTGGTGCGCCAGTGCTGGTGCGTGCCCTG	
DB	181	GAACCCCGCGGCTTTCCGCGCGCTTGGTGCGCCAGTGCTGGTGCGTGCCCTG	
QY	248	ACGCGCGCCCCCGCGCCCCCTCTTCCGCCAGGTGCTCTGCTGAGAGAGCTY	
DB	241	ACGCGCGCCCCCGCGCCCCCTCTTCCGCCAGGTGCTCTGCTGAGAGAGCTY	
QY	308	CCGAGTGTGACGAGGCTGTGCGAGCGCGCGCGAGAACGTGCTGCGCTTCGG	
DB	301	CCGAGTGTGACGAGGCTGTGCGAGCGCGCGCGAGAACGTGCTGCGCTTCGG	
QY	368	GCTGCTGAGACGGGCGCCCGCGGGGCCCCCCCCCGAGGCCCTTCACACACGAGCGTGGCG	

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GTGACCGAGTGACCGTGTGTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 907
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ACGAGGGGGCCCCCATCCACATCGGGGCCACACAGTCCCTGGGACACGCTTGTCC 1027
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CGGTGACGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1080
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CCTCCTTCTACTCAGCTCTCTGAGGCCAGCCTGACTGGCGCTCGAGGCTGTGGA 1140
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QY 1508 CAACGAA CGCGCTT CCTCAGGAA CACCAAGATT CATCTCCTCGGGAAGCJ
Db 1501 CAACGAA CGCGCTT CCTCAGGAA CACCAAGATT CATCTCCTCGGGAAGCJ
QY 1568 GCTCTCGCTG CAGGAGCTG CAGTGAAGATG AGCGTGCAGGACTG CGCTTGGC
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QY 1688 CAAAGTTCTT GCSACTG GCGTGTATG AGTGTGTAC GTCGAGCTGCT CAGGCTCTTJ
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Db 2521 CAAAGTCTTAC CTG CAGTGC CAGGGGAT CCGCAG GGGTCCATCTCT CCGAGCTT

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Db 3721 GGGCCAGCTTTTCTCTCCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGT
Qy 3788 CCAGATTGCGCATTTTTCACCCCTGCGGCTTCCCTTCTTGGCTTCCACCCCA
Db 3781 CCAGATTGCGCATTTTTCACCCCTGCGGCTTCCCTTCTTGGCTTCCACCCCA
Qy 3848 AGTGGAGAGCCCTGAGAGGAGCCCTGGAGCTCTGGGAAATTTGAGTGACCAAA
Db 3841 AGTGGAGAGCCCTGAGAGGAGCCCTGGAGCTCTGGGAAATTTGAGTGACCAAA
Qy 3908 CCTGTATACAGGCGAGGAGCCCTGCACCTGGATGGGGTCCCTTGGGTCAAAAT
Db 3901 CCTGTATACAGGCGAGGAGCCCTGCACCTGGATGGGGTCCCTTGGGTCAAAAT
Qy 3968 GAGGTGCTGTGGGAGTAAATATCTGAATATATGAGTTTTCAGTTTGAAGAAA
Db 3961 GAGGTGCTGTGGGAGTAAATATCTGAATATATGAGTTTTCAGTTTGAAGAAA

RESULT 8
AAH45901
ID AAH45901 standard; DNA; 4015 BP.
XX
AC AAH45901;
XX
DT 06-SEP-2001 (first entry)
XX
DE Human hTERT gene.
XX
KW Human; hTERT; telomerase; catalytic subunit; mRNA quantitation;
KW detection; beta-region; diagnosis; cancer; ds.
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FH Key
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2

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	2221	GG	CAGGCTCAGGAGGTGATCGCAGCATATCAAAACCCAGAAACGTTACTG
Qy	2288	TC	GTATGCCGTGGTCCAGAGGCCGCCATGGCACGTCGCGAAGGCTTCAA
Db	2281	TC	GTATGCCGTGGTCCAGAGGCCGCCATGGCACGTCGCGAAGGCTTCAA
Qy	2348	CG	CTCTACCTTGACAGACTCCAGCCGTPACATGCGACAGTTCTGTGGCTCACCT
Db	2341	CG	CTCTACCTTGACAGACTCCAGCCGTPACATGCGACAGTTCTGTGGCTCACCT
Qy	2408	GAC	CAGCCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTCTCTCTGAATGA
Db	2401	GAC	CAGCCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTCTCTCTGAATGA
Qy	2468	CAG	TGGCCTCTTCGACGCTCTTCTACGCTTCATGTCACACACGCCGTGCGCAT
Db	2461	CAG	TGGCCTCTTCGACGCTCTTCTACGCTTCATGTCACACACGCCGTGCGCAT
Qy	2528	CA	AGTCTTACGTCAGTCCAGGCGATCCCGCAGGGCTCCATCTCTCCACGCT
Db	2521	CA	AGTCTTACGTCAGTCCAGGCGATCCCGCAGGGCTCCATCTCTCCACGCT
Qy	2588	CAG	CTGTGCTACGGCGCATGGAGAAACAGTGTGTGCGGGATTCGGCGGGAT
Db	2581	CAG	CTGTGCTACGGCGCATGGAGAAACAGTGTGTGCGGGATTCGGCGGGAT
Qy	2648	GC	TCTCGCTTTGGTGGATGATTTCTTGCTGGTGACACTCACCTCACCCACCG
Db	2641	GC	TCTCGCTTTGGTGGATGATTTCTTGCTGGTGACACTCACCTCACCCACCG
Qy	2708	CT	TCTCAGGAACCTGGTCCGAGGTGTCCTTGAGTATGGCTGGTGGTGAACCT
Db	2701	CT	TCTCAGGAACCTGGTCCGAGGTGTCCTTGAGTATGGCTGGTGGTGAACCT
Qy	2768	GAC	AGTGGTAACCTTCCCTGTAGAAGACGAGCCCTGGGTGGGCACCGCTTTGT
Db	2761	GAC	AGTGGTAACCTTCCCTGTAGAAGACGAGCCCTGGGTGGGCACCGCTTTGT
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Qy	3068	CA	AGATCTCTGCTGACGGCTACAGTTTTACGATGTGTGCTGCAGCTCCCCA
Db	3061	CA	AGATCTCTGCTGACGGCTACAGTTTTACGATGTGTGCTGCAGCTCCCCA
Qy	3128	TC	CAGAGTTTGAAGAACCCACATTTTCTGGCGGTCATCTCTGACACGGCC
Db	3121	TC	CAGAGTTTGAAGAACCCACATTTTCTGGCGGTCATCTCTGACACGGCC
Qy	3188	CT	GCTACTCCATCTGAAAGCACAAGAACGACAGGATGTGCTGGGGGCCAAGGC
Db	3181	CT	GCTACTCCATCTGAAAGCACAAGAACGACAGGATGTGCTGGGGGCCAAGGC
Qy	3248	CG	GCCCTCTGCCCTCCAGGCGGTGAGTGGCTGTGCCACCAAGCATTTCTGCTC

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Qy	3968	GAGGTGCTCTGGGAGTAAATACTGAATATATAGCTTTTCAGTTTTCGAAAAA		
Db	3961	GAGGTGCTGGGAGTAAATACTGAATATATAGCTTTTCAGTTTTCGAAAAA		
RESULT 10				
ABA97534				
ID	ABA97534	standard; DNA; 4015 BP.		
XX	AC	ABA97534;		
XX	AC			
XX	XX			
DT	05-APR-2002	(first entry)		
DE	Cancer cell discrimination method related human DNA.			
XX				
KW	Human; telomerase; enzyme; cancer cell discrimination; gene;			
KW	reverse transcriptase; ds.			
XX				
OS	Homo sapiens.			
XX				
PN	JP2001309791-A.			
XX				
PD	06-NOV-2001.			
XX				
PF	02-MAY-2000; 2000JP-00138250.			
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PR	02-MAY-2000; 2000JP-00138250.			
XX				
PA	{KANE/} KANEUCHI H.			
PA	{KAMI/} KAMIMORI M.			
XX				
XX				
DR	WPI; 2002-134853/18.			
XX				
PT	Discrimination of a cancer cell in a sample tissue, comprises d			
PT	the expression level of a reverse transcriptase component of te			
PT	using a hybridization assay.			
XX				
PS	Claim 2; Page 9-10; 16pp; Japanese.			
XX				
CC	The present invention relates to a method for the discrimination			
CC	cancer cell in a sample tissue, which involves determining the			
CC	level of a reverse transcriptase component of telomerase in a c			
CC	constituting the sample tissue by an in situ hybridization of th			
CC	the enzyme, and judging a cell showing a higher expression leve			
CC	that of the reverse transcriptase component of telomerase in a			
CC	cell to be a cancer cell. The present sequence is a human DNA u			
CC	exemplification of the invention			
XX				
SQ	Sequence 4015 BP; 563 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;			
Query Match 99.3%; Score 4015; DB 6; Length 4015;				
Best Local Similarity 100.0%; Pred. No. 0;				
Matches 4015; Conservative 0; Mismatches 0; Indels 0;				
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Qy	68	GCGCGCTCCCGCTGCGCAGCGGAGCGCTGCGCTCCCTGTCGCGAGCCACTACCGCGAC		
Db	61	GCGCGCTCCCGCTGCGCAGCGGAGCGCTGCGCTCCCTGTCGCGAGCCACTACCGCGAC		
Qy	128	GCGCGTGGCAGTTGTCGCGCGCTGCGGGCCCGCAGGCGCTGCGCGCTGTGTGCA		
Db	121	GCGCGTGGCAGTTGTCGCGCGCTGCGGGCCCGCAGGCGCTGTGTGCA		
Qy	188	GGACCGCGCGGCTTTTCCGCGCGCTGTGTGCGCCGAGTGCCTGTGCTGCGTGCCTCT		

QY	3488	GAGCAGACACGAGCAGCCCTGTCTCAGCCGGGCTCTACGCTCCAGGGAGGGAGGG
DB	3481	GAGCAGACACGAGCAGCCCTGTCTCAGCCGGGCTCTACGTCCAGGGAGGGAGGG
QY	3548	CACACCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGCTTTGGCCGA
DB	3541	CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGCTTTGGCCGA
QY	3608	CATGTCGGGCTGAAGGCTGAGTGTCGGGCTGAGGCTGAGCGCTGAGCGAGTGCTCAGGCC
DB	3601	CATGTCGGGCTGAAGGCTGAGTGTCGGGCTGAGGCTGAGCGAGTGCTCAGGCCA
QY	3668	GAGTGTCAGCACACCTGCGGCTCTTCACTTCCACACAGGCTGGGCTCGGCTCC
DB	3661	GAGTGTCAGCACACCTGCGGCTCTTCACTTCCCCACAGGCTGGGCTCGGCTCC
QY	3728	GGGCCAGCTTTTCTTCCACGAGAGCCGGCTTCCACTCCCCACATGAGAAATAGT
DB	3721	GGGCCAGCTTTTCTTCCACGAGAGCCGGCTTCCACTCCCCACATGAGAAATAGT
QY	3788	CCAGATTCCGCATTGTTACCCCTCGCCCTGCCCCTTTGGCTTCCACACCCCA
DB	3781	CCAGATTCCGCATTGTTACCCCTCGCCCTGCCCTCTTTGGCTTCCACACCCCA
QY	3848	AGGTGGAGACCTTGAGAGAGGACCTTGGAGCTCTGGGAAATTTGGAGTGACCAAA
DB	3841	AGGTGGAGACCTTGAGAGAGGACCTTGGAGCTCTGGGAAATTTGGAGTGACCAAA
QY	3908	CCTGTACACAGCGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAAAT
DB	3901	CCTGTACACAGCGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAAAT
QY	3968	GAGGTGCTGGGAGTAAATACTCAATATATAGATTTTTTCAGTTTTTGAAAAA
DB	3961	GAGGTGCTGGGAGTAAATACTCAATATATAGATTTTTTCAGTTTTTGAAAAA

ACC58039
ID ACC58039 standard; cDNA: 4015 BP.

DT 11-AUG-2003 (first entry)

Telomerase reverse transcriptase; TERT; enzyme; RNA interference;
 short interfering RNA; siRNA; cancer; tumour; cytostatic; contr.
 immunosuppressive; antifertility; fungicide; antiparasitic;
 antiinflammatory; human; gene therapy; gene; ss.

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PN WO2003035667-A2.
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DE

PR 22-OCT-2001; 2001US-0345326P.

XX
44-PR1-2002; 200203-038XX
PI Rowlev PT:

XX

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2941	CGCGTTCAAAGGTGGGAGAAATGCGTGCMAAATCTTTTGGGTCTTCGGGCT	
3008	TCACAGCCTGTTTCTGGATTTGCAGGTGAACGAGCTCCAGACGGTGTGACACAA	
3001	TCACAGCCTGTTTCTGGATTTGCAGGTGAACGAGCTTCACAGACGTTGTGACCA	
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3188	CTGCTACTCCATCCTCAAGAGCCAGAGACGAGGATGTGCTGGGGGCCAAGGC	
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3248	CGGCGCTCTGCCCTCCGAGGCGTGCAGTGGTGTGCCACCAAGCATTCCTGCT	
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3308	GACTCGACACCGTGTCACTTACGTGCACTCTCTGGGGTCACTCAGACAGCCCP	
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3368	GCTGAGTCGAAAGCTCCCGGGAGACGCTGACTGCTGCCCTGGAGCCGCGACCA	
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3428	ACTGCCCTCAGACTTCAAGACCATCTGGACTCATGGCCACCCGCCACAGCCP	
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3548	CACACCGAGGCGCACCGCTGGAGTCTGAGGCTTGAGTGAAGTGTGTCGCCG	
3541	CACACCGAGGCGCACCGCTGGAGTCTGAGGCTTGAGTGAAGTGTGTCGCCG	
3608	CATCTCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTTGAGCGAGTGTCCAGCCJ	
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andard; cDNA; 4015 BP.

(first entry)

erase reverse transcriptase cDNA.

reverse transcriptase; TERT: enzyme; RNA interference; interfering RNA; siRNA; cancer; tumour; cytostatic; contraceptive; essence; antiinfertility; fungicide; antiparasitic; atory; human; gene therapy; gene; ss.

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5-A2.

; 2002WO-US033146.

; 2001US-0345326P.

2002US-0383195P.

V ROCHESTER.

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03289/38.
42063.

ic acid encoding or comprising interfering RNAs which target RNA, useful for inhibiting telomerase activity for treating infertility and disorders of the immune system.

Fig 3; 52pp; English.

sequence is that of human telomerase reverse transcriptase. The invention relates to the discovery that double-stranded RNAs, such as short interfering RNAs (siRNA), which target RNA or TERT mRNA are capable of inhibiting telomerase. Inhibition of telomerase in cancer cells leads to telomere end-to-end chromosomal fusion, and apoptosis. Interference of activity can also be used for treatment of infertility, for example on sterilisation, for immunosuppression, for treatment of viral and fungal infections, and in anti-inflammatory therapies. siRNA is active in a limited number of cell types, e.g. tumour cells, certain stem cells of the haematopoietic system, T cells, sun-damaged skin, and proliferative cervix, most normal cells not affected by telomerase RNA interference therapy.

15 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

99.3%; Score 4015; DB 7; Length 4015;

ilarity 100.0%; Pred. No. 0;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	2348	CGTCTCTACCTTTGACAGACCTCCAGCGGTCATFGCGACAGTTGCTGGCTCAAC
DB	2341	CGTCTCTACCTTTGACAGACCTCCAGCGGTCATFGCGACAGTTGCTGGCTCAAC
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DB	3181	CTGCTACTCCTCCTCAAAAGCCAAAGACGAGGGATGTGCTGGGGGCCAAGGG
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Db	1441		CGGCTTCGTGCGGGCCCTGCCTGCGCGCGCTGSGTGCCGCCCAAGGCCTCTGCGGGCTC
Qy	1508	CAACGAACGGCGCTTCCTCAGGAACACCAAGAAGTTTCATCTCCCTCGGGGAAGCG	
Db	1501	CAACGAACGGCGCTTCCTCAGGAACACCAAGAAGTTTCATCTCCCTCGGGGAAGCG	
Qy	1568	GCTCTCGCTCGAGAGCTGACGTGGAAGATGAGCGTGCGGGAATGCGCTTGGCT	
Db	1561	GCTCTCGCTCGAGAGCTGACGTGGAAGATGAGCGTGCGGGAATGCGCTTGGCT	
Qy	1628	GAGCCACAGGGTTGGCTGCTTCCGCCCGCAGAGCACCGTCTGCGTGAGAGAT	
Db	1621	GAGCCACAGGGTTGGCTGCTTCCGCCCGCAGAGCACCGTCTGCGTGAGAGAT	
Qy	1688	CAAGTTCCTGCACTGGCTGATGAGTGTGTAAGTCTGAGCTGCTCAGGTCCTTT	
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Qy	1748	TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGT	
Db	1741	TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGT	
Qy	1808	CAAGTTCGAAAGCAATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTCGGGGA	
Db	1801	CAAGTTCGAAAGCAATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTCGGGGA	
Qy	1868	GGAAGCAGAGGTCAGGCAGCATCGGAAGCCAGGCCGCGCTGCTGACGTCACAG	
Db	1861	GGAAGCAGAGGTCAGGCAGCATCGGAAGCCAGGCCGCGCTGCTGACGTCACAG	
Qy	1928	CTTCATCCCCAAGCTGACGGGCTGCGGGCGAATTGTGAACATGGACTAGCTCGT	
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Qy	1988	CAGAACGTTCCGCGAGAGAAAGAGGGCCGAGCGTCTCACTCGAGGGTGAAAGGC	
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Qy	2048	CAGCGTGCTCAACTACGAGGGGCGGGCGGCCCGGCTCTCTGGGGCGCTCTGT	
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Qy	2108	CCTGGAACGATATCCACAGGGCTTGCGGCACACTTCGTGCTGCGTGTGCGGGCCCA	
Db	2101	CCTGGAACGATATCCACAGGGCTTGCGGCACACTTCGTGCTGCGTGTGCGGGCCCA	
Qy	2168	GCCGCTGAGCTGACTTTGTCAAGTGGATGTGACGGGGCGGTACGCACCACT	
Db	2161	GCCGCTGAGCTGACTTTGTCAAGTGGATGTGACGGGGCGGTACGCACCACT	
Qy	2228	GGACAGGCTCACGGAGGTGATCGCCAGCATCATCAAACCCCAAGAACACGTA	
Db	2221	GGACAGGCTCACGGAGGTGATCGCCAGCATCATCAAACCCCAAGAACACGTA	
Qy	2288	TGCGTATGCGGTGGTCCAGNAGGCCGCCCATGGGACAGTCCGCAAGGCCCTTCAA	
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Qy	2348	CGTCTCTACCTTGACAGACTCCAGCCGTACATGCGACAGTTTCGTGGCTCACT	
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Qy	2408	GACACGCCGCTGAGGGATGCGGTGCTCATTCGAGCAGAGCTCTCTCCCTGAATGA	
Db	2401	GACACGCCGCTGAGGGATGCGGTGCTCATTCGAGCAGAGCTCTCTCCCTGAATGA	
Qy	2468	CAGTGGCTCTTCGACGCTTCTCTACGCTTCAATGTGCCACACGCGGTGCGCAT	
Db	2461	CAGTGGCTCTTCGACGCTTCTCTACGCTTCAATGTGCCACACGCGGTGCGCAT	
Qy	2528	CAAGTTCCTACGTCAGTGCCAGGGATCCCGCAGGGGCTCCATCTCTCTCCACGCT	

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TACCCAGGCGCGCACCGCTGGAGTGTGAGGCTGTGAGTGTGAGGCGCGCGCTG 3600
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QY 3668 GAGTGTCCAGCACACCTGCGCTTTCATCTTCCCCACAGGCTGGCGCTGGCTCC
Db 3661 GAGTGTCCAGCACACCTGCGCTTTCATCTTCCCCACAGGCTGGCGCTGGCTCC
QY 3728 GGGCCAGCTTTTCTCCTCACCAGAGCCCGGCTTCCACTCCCCACATAGGAATAGT
Db 3721 GGGCCAGCTTTTCTCCTCACCAGAGCCCGGCTTCCACTCCCCACATAGGAATAGT
QY 3788 CCAGATTGCCATTGTTTCACTCCCTGCGCTGCGCTTCTTTCCTTCCACCCCA
Db 3781 CCAGATTGCCATTGTTTCACTCCCTGCGCTGCGCTTCTTTCCTTCCACCCCA
QY 3848 AGTGTGAGACCTCTGAGAGGACCCCTGGGAGCTCTGGGAATTTGGAGTGACCAAA
Db 3841 AGTGTGAGACCTCTGAGAGGACCCCTGGGAGCTCTGGGAATTTGGAGTGACCAAA
QY 3908 CCTGTATACAGAGGAGGACCTTGACCTGGATGGGGTCCCTGTGGGTCAAAT
Db 3901 CCTGTATACAGAGGAGGACCTTGACCTGGATGGGGTCCCTGTGGGTCAAAT
QY 3968 GAGGTGCTGTGGAGTAAATACTGAATATATGAGTTTTCAGTTTGAATAAA
Db 3961 GAGGTGCTGTGGAGTAAATACTGAATATATGAGTTTTCAGTTTGAATAAA

RESULT 14

ACC44482
ID ACC44482 standard; DNA; 4015 BP.
XX
AC ACC44482;
XX
DT 29-AUG-2003 (first entry)
XX Human telomerase reverse transcriptase gene.
DE
KW Gene; ds; human; telomerase reverse transcriptase; adipogenic c
KW primary preadipocyte cell; adipogenesis; obesity; adipocytokine
KW anorectic; adiponectin; insulin.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 56..3454
FT /*tag= a
FT /product= "telomerase reverse transcriptase"
XX
PN WO2003031640-A2.
XX
PD 17-APR-2003.
XX
PF 07-OCT-2002; 2002WO-US031635.
XX
PR 06-OCT-2001; 2001US-0327650P.
PR 06-OCT-2001; 2001US-0327651P.
XX
PA (BOST-) BOSTON MEDICAL CENT CORP.
XX
PI Kirkland J, Tchekonia T;
XX
DR WPI; 2003-421278/39.
DR P-PSDB; ABR58045.
XX
PT New primary preadipocyte strain expressing telomerase reverse
PT transcriptase, useful in research applications, screening assay;
PT clinical applications, and in the administration of therapeutic
PT particularly for obesity.
XX
PS Disclosure; Page 11-13; 53pp; English.
XX
CC The invention relates to the generation of primary preadipocyte
CC strains that express telomerase reverse transcriptase (TERT-
CC catalytic subunit of telomerase), and maintain and/or enhance r

und maintain adipogenic capacity of the cell. This sequence the gene encoding the TRP protein. The cell strain can be search to study all aspect of adipogenesis, especially in researching treatments for e.g. obesity. The cell can also be identify adipogenesis modulators for use as therapeutic agents mones, growth factors, cytokines, enzymes, cholesterol binding cholesterol removing proteins or their combinations. ly, the therapeutic agent may be an adipocytokine, preferably, or insulin

15 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

99.3%; Score 4015; DB 7; Length 4015;

Identity	100.0%	Fred. NO. 0;			
Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;				

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AGCGTCGGTCTGCTGCCCAAGTGGGAAGCCCTGGCCCGGGCAACCCCGCGATGCC 50

'GGGCTCCCCGGTGGCCGAGCGGTGGGTCCTCTGCTGGCGACCACTA CCCCAGCCTCAT

GGGCTCCCGGTGCAGCGCTCCTCTCCGCCAATACCGCCGCGCCG

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Db	901	CACCTCTTTGGAGGTGGCTCTCTGGCAGCGCCACTCCCACCCACTCCGTGG	
Qy	968	GCACACGGGGCCCCCATCCACATCGCGGCCACACACTCTCCCTGGGACAACG	
Db	961	GCACACGGGGCCCCCATCCACATCGCGGCCACACACTCTCCCTGGGACAACG	
Qy	1028	CCGGTGTACGCGAGACCAAGCACTTCTCTACTCTCTCAGGGCAACAAGAGC	
Db	1021	CCGGTGTACGCGAGACCAAGCACTTCTCTACTCTCTCAGGGCAACAAGAGC	
Qy	1088	GCCCTCCTCTACTCAGCTCTCTGAGGCCAGCGCTGACTGGCGCTCGAGGCT	
Db	1081	GCCCTCCTCTACTCAGCTCTCTGAGGCCAGCGCTGACTGGCGCTCGAGGCT	
Qy	1148	GACCATCTTCTGGGTTTCAGGCCCTCGATGCCAGGGACTCCCGCAGGTTGCC	
Db	1141	GACCATCTTCTGGGTTTCAGGCCCTCGATGCCAGGGACTCCCGCAGGTTGCC	
Qy	1208	GCCCACGGCTACTGGCAATGCGGCCCTGTCTTCTGGAGCTGCTTGGGAAACA	
Db	1201	GCCCACGGCTACTGGCAATGCGGCCCTGTCTTCTGGAGCTGCTTGGGAAACA	
Qy	1268	GTGCCCTCAGGGGTGCTCTCAAGACGACACTGCCCGCTGCAGCTGCGGTCA	
Db	1261	GTGCCCTCAGGGGTGCTCTCTAAGACGACACTGCCCGCTGCAGCTGCGGTCA	
Qy	1328	AGCGGTGTCTGTGCCCGGAGAGGCCACAGGCTCTGTGGCGGCCCGCCAGGA	
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Qy	1388	CACAGACCCCGCTGGTGAGTGTCTGCCCAGCACAGCAGCCCTCTGGCA	
Db	1381	CACAGACCCCGCTGGTGAGTGTCTGCCCAGCACAGCAGCCCTCTGGCA	
Qy	1448	CGCTTCTGTCGGGCTGCTCGCGCGGTGTGTGCGCCCGCAGGCTCTGGGGCT	
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Qy	1568	GCTCTCGTGCAGGAGCTGACGTGGAAGATGAGCGTGCAGGACTGCGCTTGGC	
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Qy	1628	GAGCCAGAGGTGGCTGTCTTCCGCGCAGAGCACGCTGCTGCTGAGGAGAT	
Db	1621	GAGCCAGAGGTGGCTGTCTTCCGCGCAGAGCACGCTGCTGCTGAGGAGAT	
Qy	1688	CAAGTTCTCTGCACTGGCTGATGAGTGTGTACGTCTGAGCTGCTCAGTCTTT	
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Qy	1748	TGTCAAGGAGACACAGTTTCAAGAAACAGGCTCTTTTCTACCGGAAGAGTGT	
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Qy	1808	CAAGTTGCAAGACATTGGAAATCAGACAGCACTTGAAGGGTGCAGCTGCCGGA	
Db	1801	CAAGTTGCAAGACATTGGAAATCAGACAGCACTTGAAGGGTGCAGCTGCCGGA	
Qy	1868	GGAAGCAGAGGTGAGGACGATCGGGAAGCCAGGCGCCGCTGCTGAGCTCCAG	
Db	1861	GGAAGCAGAGGTGAGGACGATCGGGAAGCCAGGCGCCGCTGCTGAGCTCCAG	
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DT	17-JAN-2000 (first entry)

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	ase reverse transcriptase; hTRT; telomerase; hEST2; rotein component; cell proliferative capacity; ality; neoplastic phenotype; diagnostic application; application; telomerase related condition; cancer; agent; telomerase expression; telomerase activity; ds.		
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	ynucleotides for human telomerase reverse transcriptase used ing or treating cancer.		
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	sequence encodes for human telomerase reverse transcriptase s is the catalytic protein component of telomerase and is also as hEST2. This correlates with cell proliferative capacity, activity, and the development of a neoplastic phenotype. Human se oligonucleotides are useful for diagnostic or prognostic s to telomerase related conditions, including cancer. They are as therapeutic agents, for inhibition of telomerase and activity		
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; Sequence 343, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
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; CLASSIFICATION: 536
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; APPLICATION NUMBER: US 08/911,312
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13 Application US/09402181B
14 839
15 INVENTION:
16 INVENTOR: Cech, Thomas R.
17           Lingner, Joachim
18           Nakamura, Toru
19           Chapman, Karen B.
20           Morin, Gregg B.
21           Harley, Calvin B.
22           Andrews, William H.
23 INVENTION: Human Telomerase Catalytic Subunit
24 OF SEQUENCE: 633
25 REFERENCE: Townsend and Townsend and Crew LLP
26 REF: Two Embarcadero Center, Eighth Floor
27 SF: San Francisco
28 STATE: California
29 COUNTRY: USA
30 94111-3834
31 READABLE FORM:
32 DISC TYPE: Floppy disk
33 COMPUTER: IBM PC Compatible
34 OPERATING SYSTEM: PC-DOS/MS-DOS
35 SOFTWARE: Patent In Release #1.0, Version #1.30
36 APPLICATION DATA:
37 APPLICATION NUMBER: US/09402,181B
38 FILING DATE: 29-Sep-1997
39 CLASSIFICATION: <Unknown>
40 APPLICATION DATA:
41 APPLICATION NUMBER: US 08/724,643
42 FILING DATE: 01-OCT-1996
43 APPLICATION NUMBER: US 08/844,419
44 FILING DATE: 18-APR-1997
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46 FILING DATE: 25-APR-1997
47 APPLICATION NUMBER: US 08/851,843
48 FILING DATE: 06-MAY-1997
49 APPLICATION NUMBER: US 08/854,050
50 FILING DATE: 09-MAY-1997
51 APPLICATION NUMBER: US 08/911,312
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55 APPLICATION NUMBER: US 08/915,503
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57 APPLICATION NUMBER: WO PCT/US97/17885
58 FILING DATE: 01-OCT-1997
59 AGENT INFORMATION:
60 NAME: Ausenhus, Scott L.
61 STRATION NUMBER: 42,271
62 REFERENCE/DOCKET NUMBER: 015389-002620US
63 COMMUNICATION INFORMATION:
64 TELEPHONE: (415) 576-0200
65 TELEFAX: (415) 576-0300
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Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-Nov. 6617110-2000
CLASSIFICATION: <Unknown>
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APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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RESULT 4
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; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809el.7
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: Two Embarcadero Center,
; CITY: San Francisco, CA 94111-4202
; COUNTRY: US

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Location US/08974549A

178

ATTN:

Cech, Thomas R.

Lingner, Joachim

Yakamura, Toru

Chapman, Karen B.

Marin, Gregg B.

Harley, Calvin B.

Andrews, William H.

ENTION: Human Telomerase Catalytic Subunit

SEQUENCES: 727

IE ADDRESS:

Townsend and Townsend and Crew LLP

Embarcadero Center, Eighth Floor

San Francisco

California

USA

-3834

TABLE FORM:

IBM PC compatible

SYSTEM: PC-DOS/MS-DOS

Patent In Release #1.0, Version #1.30

LOCATION DATA:

NUMBER: US/08/974,549A

FILE: 19-NOV-1997

FILE: 536

ATTION DATA:

NUMBER: US 08/724,643

FILE: 01-OCT-1996

ATTION DATA:

NUMBER: US 08/844,419

FILE: 18-APR-1997

ATTION DATA:

NUMBER: US 08/846,017

FILE: 25-APR-1997

ATTION DATA:

NUMBER: US 08/851,843

FILE: 06-MAY-1997

ATTION DATA:

NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
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TOPOLOGY: linear
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transcriptase (hTRT) catalytic protein
component"
US-08-974-549A-1

Query Match

Best Local Similarity 99.3%; Score 4015; DB 3; Length 4015;

Matches 4015; Conservative 0; Mismatches 0; Indels 0;

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US-08-854-050-224		
; Sequence 224, Application US/08854050		
; Patent No. 6261836		
; GENERAL INFORMATION:		
; APPLICANT: Cech, Thomas R.		
; APPLICANT: Lingner, Joachim		
; APPLICANT: Nakamura, Toru		
; APPLICANT: Chapman, Karen B.		
; APPLICANT: Morin, Gregg B.		
; APPLICANT: Harley, Calvin		
; APPLICANT: Andrews, William H.		
; TITLE OF INVENTION: No. 6261836el Telomerase		
; NUMBER OF SEQUENCES: 225		
; CORRESPONDENCE ADDRESS:		
; ADDRESSEE: Townsend and Townsend and Crew LLP		
; STREET: Two Embarcadero Center, 8th Floor		
; CITY: San Francisco		
; STATE: California		
; COUNTRY: United States of America		
; ZIP: 94111		
; COMPUTER READABLE FORM:		
; MEDIUM TYPE: Floppy disk		
; COMPUTER: IBM PC compatible		
; OPERATING SYSTEM: PC-DOS/MS-DOS		
; SOFTWARE: PatentIn Release #1.0, Version #1.30		
; CURRENT APPLICATION DATA:		
; APPLICATION NUMBER: US/08/854,050		
; FILING DATE: 09-MAY-1997		
; CLASSIFICATION: 536		
; PRIOR APPLICATION DATA:		
; APPLICATION NUMBER: US 08/851,843		
; FILING DATE: 06-MAY-1997		
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; PRIOR APPLICATION DATA:		
; APPLICATION NUMBER: US 08/846,017		
; FILING DATE: 25-APR-1997		
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; PRIOR APPLICATION DATA:		
; APPLICATION NUMBER: US 08/844,419		
; FILING DATE: 18-APR-1997		
; CLASSIFICATION: 536		
; PRIOR APPLICATION DATA:		
; APPLICATION NUMBER: US 08/724,643		
; FILING DATE: 01-OCT-1996		
; CLASSIFICATION: 536		
; ATTORNEY/AGENT INFORMATION:		
; NAME: Apple, Randolph T.		
; REGISTRATION NUMBER: 36,429		
; REFERENCE/DOCKET NUMBER: 015389-002930US		
; TELECOMMUNICATION INFORMATION:		
; TELEPHONE: (415) 576-0200		
; TELEFAX: (415) 576-0300		

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RESULT 7

US-09-430-323-224

; Sequence 224, Application US/09430323

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location US/09572423B
399
TION:
Brett P. Monia
William A. Gaarde
ward Wancewicz
TION: ANTISENSE MODULATION OF TERT EXPRESSION
.: ISPH-0462
ATION NUMBER: US/09/572.423B
; DATE: 2000-05-16
ID NOS: 29

o sapiens
}
): ... (3454)

99.3%; Score 4015; DB 4; Length 4015;
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Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AGCGTTCGCTCTGCTGCGCAGTGGGAAGCCCTGGCCCGCGCCACACCCCGCGATGCC 60

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[illegible]

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Db	2821	GC	CGG	CC	CAG	CG	CTA	T	CC
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; EARLIER APPLICATION NUMBER: US 08/974,584	
; EARLIER FILING DATE: 1997-11-19	
; EARLIER APPLICATION NUMBER: US 09/052,864	
; EARLIER FILING DATE: 1998-03-31	
; NUMBER OF SEQ ID NOS: 21	
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; SEQ ID NO 1	
; LENGTH: 4015	
; TYPE: DNA	
; ORGANISM: Homo sapiens	
; FEATURE:	
; NAME/KEY: CDS	
; LOCATION: (56)..(3454)	
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT)	
US-09-128-354-1	
Query Match 99.3%; Score 4015; DB 4; Length 4015;	
Best Local Similarity 100.0%; Pred. No. 0;	
Matches 4015; Conservative 0; Mismatches 0; Indels 0;	
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Publication US/09128354

7200

ATION:

in, Gregg B.

on, Corporation

ATION: Human Telomerase Catalytic Subunit Variants

015389-003310US

ATION NUMBER: US/09/128,354

DATE: 1998-08-03

ATION NUMBER: US 08/851,843

DATE: 1997-05-06

ATION NUMBER: US 08/854,050

DATE: 1997-05-09

ATION NUMBER: US 08/911,312

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QY
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Db	1801	CAAGTTCCAAAGCATTTGGAAATCAGACAGCACATTGAGAGGGTGACGTGCGGGA
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RESULT 11
US-09-052-919-1
Sequence 1, Application US/09052919
Patent No. 644650
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Hatley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Antisense Compositions for Detecting and
TITLE OF INVENTION: Inhibiting Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,919
FILING DATE: 31-MAR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

```

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ent, Annette S.
ON NUMBER: 42,058
DOCKET NUMBER: 015389-003600US
ATION INFORMATION:
(415) 576-0200
(415) 576-0300
R SEQ ID NO: 1:
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linear
E: CDNA

CDS
56..3454
RMATION: /product= "human telomerase reverse
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99.3%; Score 4015; DB 4; Length 4015;
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P
C

Publication US/08912951
1789

INVENTOR:

Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin

Andrews, William H.

INVENTOR: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS

SEQUENCES: 335

CE ADDRESS:

Townsend and Townsend and Crew LLP
Embarcadero Center, 8th Floor

San Francisco

California

United States of America

1

DABLE FORM:

E: Floppy disk

IBM PC compatible

SYSTEM: PC-DOS/MS-DOS

PatentIn Release #1.0, Version #1.30

ICATION DATA:

N NUMBER: US/08/912,951

E: 14-AUG-1997

ATION DATA:

ATION DATA:

N NUMBER: US 08/854,050

E: 09-MAY-1997

ATION DATA:

ATION DATA:

N NUMBER: US 08/851,843

E: 06-MAY-1997

ATION DATA:

ATION DATA:

N NUMBER: US 08/846,017

E: 25-APR-1997

ATION DATA:

ATION DATA:

N NUMBER: US 08/844,419

E: 18-APR-1997

ATION DATA:

ATION DATA:

N NUMBER: US 08/724,643

E: 01-OCT-1996

ATION DATA:

ATION DATA:

le, Randolph T.

DN NUMBER: 36,429

DOCKET NUMBER: 015389-002600US

ATION INFORMATION:

(415) 576-0200

(415) 576-0300

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3: CDNA

CDS

56..3454

INATION: /product= "hTERT"

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INATION: transcriptase (hTERT) catalytic protein

OTHER INFORMATION: component "

US-08-912-951-1

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3ACGTTTCCGAGAGAAAGGCGCGAGCTCTCACCTCGAGGGTGAAGGCACTGTT 2040

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3CGTCTCAACTACAGCGGGCGCGGGCGGCCCGGCTCTTGGCGGCTCTGTGCTGGG 2100

QY	2108	CCTGGA	CGATAT	TCACA	GGGCGT	TGGCGCA	CC	TTTGC	CTGCGT	GTGCGG	CCGCA	
DB	2101	CCTGGA	CGATAT	TCACA	GGGCGT	TGGCGCA	CC	TTTGC	CTGCGT	GTGCGG	CCGCA	
QY	2168	GCCGCT	GAGCTG	TACTTT	CTCA	AGGTGG	ATGTGA	CGGG	CGGT	TACGA	CACCAT	
DB	2161	GCCGCT	GAGCTG	TACTTT	CTCA	AGGTGG	ATGTGA	CGGG	CGGT	TACGA	CACCAT	
QY	2228	GGACAG	GGCTCA	CGGAGG	TCA	TCGCC	AGCATCA	TCAA	ACCC	AGAA	CCGTA	CTG
DB	2221	GGACAG	GGCTCA	CGGAGG	TCA	TCGCC	AGCATCA	TCAA	ACCC	AGAA	CCGTA	CTG
QY	2288	TCGGTA	TGCGGT	TGCCAG	AAGCG	CGCCCA	TGGG	CACG	TCGCG	AAGGCC	CTTCAA	
DB	2281	TCGGTA	TGCGGT	TGCCAG	AAGCG	CGCCCA	TGGG	CACG	TCGCG	AAGGCC	CTTCAA	
QY	2348	CGTCTC	TACCTT	GACAG	ACCTCC	CAGCGG	TACATG	CGAC	CAGTTC	GTGGCT	CACCT	
DB	2341	CGTCTC	TACCTT	GACAG	ACCTCC	CAGCGG	TACATG	CGAC	CAGTTC	GTGGCT	CACCT	
QY	2408	GACCAG	CGCGGT	GAGGGA	TCCGTG	TCATC	GAGCA	GAGG	TCCTC	CTGAAT	TGA	
DB	2401	GACCAG	CGCGGT	GAGGGA	TCCGTG	TCATC	GAGCA	GAGG	TCCTC	CTGAAT	TGA	
QY	2468	CAGTGG	CGCTCT	TGACG	AGCTCT	CTC	TACG	CTTCA	TGTC	CCAC	CGCGT	CGCAT
DB	2461	CAGTGG	CGCTCT	TGACG	AGCTCT	CTC	TACG	CTTCA	TGTC	CCAC	CGCGT	CGCAT
QY	2528	CAAGTCT	CAGTCC	AGTGC	AGGGAT	TC	CGCAG	GGCTCC	ATCTC	CTCTC	TCAC	CGCT
DB	2521	CAAGTCT	CAGTCC	AGTGC	AGGGAT	TC	CGCAG	GGCTCC	ATCTC	CTCTC	TCAC	CGCT
QY	2588	CAGCCT	GTGCTC	AGCGG	ACATG	GAGAA	CAAG	CTGTTT	GCGG	GGATTC	CGCGGG	GA
DB	2581	CAGCCT	GTGCTC	AGCGG	ACATG	GAGAA	CAAG	CTGTTT	GCGG	GGATTC	CGCGGG	GA
QY	2648	GCTCCT	CGCTTT	GGTGG	ATGATTT	CTTGT	TGGTGA	CACCTC	ACCTC	ACCC	ACGCG	
DB	2641	GCTCCT	CGCTTT	GGTGG	ATGATTT	CTTGT	TGGTGA	CACCTC	ACCTC	ACCC	ACGCG	
QY	2708	CTTCTC	TGACG	ACCTCG	TCCG	AGGTGT	TCCTC	GAGTAT	TGCTC	CGTGGT	GAACTT	
DB	2701	CTTCTC	TGACG	ACCTCG	TCCG	AGGTGT	TCCTC	GAGTAT	TGCTC	CGTGGT	GAACTT	
QY	2768	GACAGT	GGTGAA	CTTCC	CTGTAGA	AGACG	AGCCCT	TGGGTG	GCAC	CGGCTTT	TGT	
DB	2761	GACAGT	GGTGAA	CTTCC	CTGTAGA	AGACG	AGCCCT	TGGGTG	GCAC	CGGCTTT	TGT	
QY	2828	GCGGG	CCACG	GGCTAT	TCCCT	TGTTGG	TGGG	CCCTG	CTGTG	GATAT	CCCGGA	CCCTT
DB	2821	GCGGG	CCACG	GGCTAT	TCCCT	TGTTGG	TGGG	CCCTG	CTGTG	GATAT	CCCGGA	CCCTT
QY	2888	GCAGAG	CGCAT	TACTC	CAGCTAT	TGCC	CGGAC	CTCC	ATC	AGAG	CCAGTCT	CACCTT
DB	2881	GCAGAG	CGCAT	TACTC	CAGCTAT	TGCC	CGGAC	CTCC	ATC	AGAG	CCAGTCT	CACCTT
QY	2948	CGGCTT	CAAGG	CTGGAG	GAA	CA	TGCTG	TCGAAA	CTCTTT	GGGGT	CTTTG	CGGCTT
DB	2941	CGGCTT	CAAGG	CTGGAG	GAA	CA	TGCTG	TCGAAA	CTCTTT	GGGGT	CTTTG	CGGCTT
QY	3008	TCACAG	CGCTTT	CTGGA	TTTTCG	AGGTGA	AGCCTC	CCAG	ACG	GTGTG	TCACAA	
DB	3001	TCACAG	CGCTTT	CTGGA	TTTTCG	AGGTGA	AGCCTC	CCAG	ACG	GTGTG	TCACAA	
QY	3068	CAAGAT	CTCT	CTGCTG	CA	GGCGG	CTA	CAGG	TTTTC	ACG	CGATGT	GTG
DB	3061	CAAGAT	CTCT	CTGCTG	CA	GGCGG	CTA	CAGG	TTTTC	ACG	CGATGT	GTG
QY	3128	TCAGCA	AGTTT	TGGA	GAA	CCCC	CACA	ATTTTT	TCTG	CGCGT	CA	TCT
DB	3121	TCAGCA	AGTTT	TGGA	GAA	CCCC	CACA	ATTTTT	TCTG	CGCGT	CA	TCT

Db	1981	 CAGAA CGTTCCG CAGAAAAAGAGGGCGCAGCGTCTCACCTCGAGGGTGAAGG
Qy	2048	CAGCGTGTCTAACTACGAGCGGGCGCGCGCCCGGCTCTCTGGCGGCTCTCTG
Db	2041	CAGCGTGTCTAACTACGAGCGGGCGCGCGCCCGGCTCTCTGGCGGCTCTCTG
Qy	2108	CCTGGA CGATATCCACAGGGGCTTGGCGCACCTTCGTCTGCTGCTGCGGGGCC
Db	2101	CCTGGA CGATATCCACAGGGGCTTGGCGCACCTTCGTCTGCTGCTGCGGGGCC
Qy	2168	GCCGCTTGAGCTGTACTTTGTCAAGGTGGATGTGA CGGGCGGCTACGACCA
Db	2161	GCCGCTTGAGCTGTACTTTGTCAAGGTGGATGTGA CGGGCGGCTACGACCA
Qy	2228	GGACAGGCTCACGGAGGTCAATCGGCAGCATCATCAACCCCGAGNACAGTACTT
Db	2221	GGACAGGCTCACGGAGGTCAATCGGCAGCATCATCAACCCCGAGNACAGTACTT
Qy	2288	TCGGTATCCGCTGTCTCAGAAAGCCGCCATGGGCAGCTCGCGAAGGCTTCAJ
Db	2281	TCGGTATGCGGTGTCTCCAGAAAGCCGCCATGGGCAGCTCGCGAAGGCTTCAJ
Qy	2348	CGTCTCTACCTTGACAGACCTCCAGCCGTAATATGCGACAGTTCTGTGCTCACCT
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Qy	2408	GACCAGCCCGCTGAGGGATGCGGTGCTCATTCGACAGAGAGTCTCTCCCTGAATG
Db	2401	GACCAGCCCGCTGAGGGATGCGGTGCTCATTCGACAGAGAGTCTCTCCCTGAATG
Qy	2468	CAGTGGGCTCTTTCGACGTCTTCTCTAGCTTTCATGTGCGACACGCGCTGCGCAJ
Db	2461	CAGTGGGCTCTTTCGACGTCTTCTCTAGCTTTCATGTGCGACACGCGCTGCGCAJ
Qy	2528	CAAGTCTCAGTCCAGTCCAGGGATCCCGCAGGGCTCCATCTCTTCCACGCT
Db	2521	CAAGTCTCAGTCCAGTCCAGGGATCCCGCAGGGCTCCATCTCTTCCACGCT
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Qy	2708	CTTCTCTCAGAACCTTGTCGAGGTCTCCTCGAGTATGCTGCTGGTGGTGAACCTT
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Qy	2768	GACAGTGGTGAACCTTCCCTGTGAGAAGCAGGCGCCTGGGTGGCAGCGCTTTGT
Db	2761	GACAGTGGTGAACCTTCCCTGTGAGAAGCAGGCGCCTGGGTGGCAGCGCTTTGT
Qy	2828	GCCGGCCACGGCCTATTCCTCTGTGTGCGGCTGTCTGTGATACCCGACCCCT
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1243 GGCAGGCTCAGCGAGTCACTGCGCAGCATCATCAAAACCCAGAACACGCTACTG 2221

3361	Db	GCTGAGTCGAAAGCTCCCGGGACACGCTGACTGCTGCCCTGGAGGCGCAGGCCAA
3428	Qy	ACTGCCCTCAGACTTCAAGACCAATCCTCGACTGATGGCCACCCGCCACAGCCA
3421	Db	ACTGCCCTCAGACTTCAAGACCAATCCTCGACTGATGGCCACCCGCCACAGCCA
3488	Qy	GAGCAGACACGAGCCCTGTCAAGCCCGGCTCTACGTCCAGGGAGGGAGGG
3481	Db	GAGCAGACACGAGCCCTGTCAAGCCCGGCTCTACGTCCAGGGAGGGAGGG
3548	Qy	CACACCCAGGCCCGCACCGCTGGAGTCTGAGGCTGAGTCAAGTGTTTGGCCGAI
3541	Db	CACACCCAGGCCCGCACCGCTGGAGTCTGAGGCTGAGTCAAGTGTTTGGCCGAI
3608	Qy	CATGTCGGCTGAAGGCTGAGTGTCGGCTGAGGCTGAGGAGTGTCAGGCCAJ
3601	Db	CATGTCGGCTGAAGGCTGAGTGTCGGCTGAGGCTGAGGAGTGTCAGGCCAJ
3668	Qy	GAGTGTCCAGCACACCTGCCGCTCTTCACTCCCCACAGGCTGGCGCTCGGCTCC
3661	Db	GAGTGTCCAGCACACCTGCCGCTCTTCACTCCCCACAGGCTGGCGCTCGGCTCC
3728	Qy	GGGCAGGCTTTTCTCAACAGGCGCGCTTCCACTCCCAACATAGGAAATAGT
3721	Db	GGGCAGGCTTTTCTCAACAGGCGCGCTTCCACTCCCAACATAGGAAATAGT
3788	Qy	CCAGATTCCGCAATGTTTCAACCCCTCGCCCTGCTTGGCTTCCACCCCA
3781	Db	CCAGATTCCGCAATGTTTCAACCCCTCGCCCTGCTTGGCTTCCACCCCA
3848	Qy	AGTGGAGACCTTGAGAGGACCTTGGAGCTCTGGGAAATTTGGAGTGACCAAA
3841	Db	AGTGGAGACCTTGAGAGGACCTTGGAGCTCTGGGAAATTTGGAGTGACCAAA
3908	Qy	CCCTGTACACAGGCGAGGACCCCTGCACCTGATGGGGTCCCTGTGGGTCAAAAT
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3968	Qy	GAGTGTCTGGGAGTAAATACATGAATATATGAGTTTTTTCAGTTTTGAAAAA
3961	Db	GAGTGTCTGGGAGTAAATACATGAATATATGAGTTTTTTCAGTTTTGAAAAA

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US-09-721-436-1
Sequence 1, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09721456
FILING DATE: 22-No. 6617110-2000

Db	30.1	CCGAGTGTCTGCAGAGGCTGTGTGAGCGGGCGCGAAGAACGTGTCTGGCCCTTCGG	
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SUMMARIES

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99.3	4015	9	US-09-733-294A-3	Sequence 3, Appli	
99.3	4015	9	US-09-990-080-1	Sequence 1, Appli	
99.3	4015	9	US-09-843-676-224	Sequence 224, App	
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99.3	4015	13	US-10-449-565-1	Sequence 1, Appli	
99.3	4015	15	US-10-053-758-224	Sequence 224, App	
99.3	4015	15	US-10-208-243-1	Sequence 1, Appli	
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99.3	4015	15	US-10-054-611-224	Sequence 224, App	
99.3	4015	15	US-10-105-963-1	Sequence 1, Appli	
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ALIGNMENTS

RESULT 1
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Sequence 343, Application US/10325810
Publication No. US20030204069A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997

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 .AGCAGAGTTCAGGACAGCATCCGGAAGCCAGACCGCGCCCTGCTGACGTCCAGACTCCG 1927
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 .AAGCTTCGCAGAGAAAGAGGGCCGAGCGTCTCACCTCGAGGGGTGAAGGCACGTGT 2047
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 .GTCTCTACGTTCAGTGCCAGGGGATCCCGCAGGGTCTCATCTCTTCCACGCTGCTGTG 2587

Db	2521	CAAGTCCTACGTCCTCAGTCGCCAGGGGATCCCGCAGGSGCTCCATCTCTCTCCACGCTC
Qy	2588	CAGCCTGTGCTACGGCGGACATGGAGAACCAAGCTGTTTCGGGGGATTCGGCGGG
Dd	2581	CAGCCTGTGCTACGGCGGACATGGAGAACCAAGCTGTTTCGGGGGATTCGGCGGG
Qy	2648	GCTCCTGCGTTTGGTGGATGATTTCTTGTTGTGTGACACCTCACCTCACCACGCG
Dd	2641	GCTCCTGCGTTTGGTGGATGATTTCTTGTTGTGTGACACCTCACCTCACCACGCG
Qy	2708	CTTCTCTCAGAACCCCTGGTCCGAGGTGTCCCTGAGTATGTGCTGCGTGTGTGAACCTT
Dd	2701	CTTCTCTCAGAACCCCTGGTCCGAGGTGTCCCTGAGTATGTGCTGCGTGTGTGAACCTT
Qy	2768	GACAGTGGTGAACTTCCCTGTGTAAGACGAGGSCCTGGTGGCGATCCGCGCTTTTGT
Dd	2761	GACAGTGGTGAACTTCCCTGTGTAAGACGAGGSCCTGGTGGCGATCCGCGCTTTTGT
Qy	2828	GCCGGGCCACGGGCTATTCCCTCTGGTGGGCGCTGCTGTGATATCCCGGACCCCTT
Dd	2821	GCCGGGCCACGGGCTATTCCCTCTGGTGGGCGCTGCTGTGATATCCCGGACCCCTT
Qy	2888	GCGAGGGACTACTCAGCTATGCCCCGGACCTCCATCAGACGCCAGTCTCACCTT
Dd	2881	GCGAGGGACTACTCAGCTATGCCCCGGACCTCCATCAGAGCCAGTCTCACCTT
Qy	2948	CGGCTTCAAGGCTGGGAGAAATCGGTCGGAACTCTTTGGGGCTCTTGCGGCT
Dd	2941	CGGCTTCAAGGCTGGGAGAAATCGGTCGGAACTCTTTGGGGCTCTTGCGGCT
Qy	3008	TCACAGCCTGTTTCTGGATTTTCAGAGGTGAAACAGCCTCCAGACGGTGTGCCACCAAC
Dd	3001	TCACAGCCTGTTTCTGGATTTTCAGAGGTGAAACAGCCTCCAGACGGTGTGCCACCAAC
Qy	3068	CAGATCTCTCTGCTGCGAGGCGTAAGGTTTCAACGATGTGTGTGAGTCTCCF
Dd	3061	CAGATCTCTCTGCTGCGAGGCGTAAGGTTTCAACGATGTGTGTGAGTCTCCF
Qy	3128	TCAGCAAGTTTCGAGAACCCACATTTTCTCGGGTCTATCTCTGACACGGC
Dd	3121	TCAGCAAGTTTCGAGAACCCACATTTTCTCGGGTCTATCTCTGACACGGC
Qy	3188	CTGCTACTCCATCCTGAAAGCCAAACGACGGGATGTGCTGGGGGCCAAGGGC
Dd	3181	CTGCTACTCCATCCTGAAAGCCAAACGACGGGATGTGCTGGGGGCCAAGGGC
Qy	3248	CGGCGCTCTGCGCTCTGAGGCCGTGCGATGTGCTGTGCCACCAAGATTTCTGTCT
Dd	3241	CGGCGCTCTGCGCTCTGAGGCCGTGCGATGTGCTGTGCCACCAAGATTTCTGTCT
Qy	3308	GACTCGACACCGTGTCACTAGTGCCACTCCTGGGGTCACTCAGGACAGCCGAG
Dd	3301	GACTCGACACCGTGTCACTAGTGCCACTCCTGGGGTCACTCAGGACAGCCGAG
Qy	3368	GCTGAGTCGGAAAGCTCCCGGGGACGACGCTGACCTGCGCTTGAGGCCCGCAGCCAAC
Dd	3361	GCTGAGTCGGAAAGCTCCCGGGGACGACGCTGACCTGCGCTTGAGGCCCGCAGCCAAC
Qy	3428	ACTGCGCCTCAGACTTCAAGACATCCTGGACTGTGATGCGCACCCGCGCCACAGCCAG
Dd	3421	ACTGCGCCTCAGACTTCAAGACATCCTGGACTGTGATGCGCACCCGCGCCACAGCCAG
Qy	3488	GAGCAGACACGAGCCCTGTGACGCGGGCTCTAGTCCGAGGAGGAGGGGG
Dd	3481	GAGCAGACACGAGCCCTGTGACGCGGGCTCTAGTCCGAGGAGGAGGGGG
Qy	3548	CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCGCTGAGTGTGTTTGGCCGAG
Dd	3541	CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCGCTGAGTGTGTTTGGCCGAG
Qy	3608	CATGTCGGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGCAGTGTCCAGCCAA
Dd	3601	CATGTCGGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCAGTGTCCAGCCAA

[illegible]

Qy	2468	CAGTGGCCTCTTCGACGTCCTTCCCTACGCTTTCATGTGCCACCAACGCCGCTGGCGGCA
Db	2461	CAGTGGCCTCTTCGACGTCCTTCCCTACGCTTTCATGTGCCACCAACGCCGCTGGCGCAT
Qy	2528	CAAGTCTCTACGTCACGTCGACAGGGATCCCGCAGAGGCTCCATCTCTCTCCACGCT
Db	2521	CAAGTCTCTACGTCACGTCGACAGGGATCCCGCAGAGGCTCCATCTCTCTCCACGCT
Qy	2588	CAGCCTGTGCTACGGCGACATCGAGAAACAGCTGTTTGGGGGGAATTCGGCGGGAA
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Qy	2648	GCTCCTCGCTTGTGGTGATGATTTCTTGTGTGACACTCACTACCTCAACCCACGC
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Qy	2708	CTTCTCTCAGAACCTCGTCCGAGGTGTCTCTGAGTATGGCTGCGTGGTGAACATTT
Db	2701	CTTCTCTCAGAACCTCGTCCGAGGTGTCTCTGAGTATGGCTGCGTGGTGAACATTT
Qy	2768	GACAGTGTGAACTTCCCTGTAGAGACGAGGCCCTGGGTGCGACGGCTTTTGT
Db	2761	GACAGTGTGAACTTCCCTGTAGAGACGAGGCCCTGGGTGCGACGGCTTTTGT
Qy	2828	GCCGGCCACCGGCTATTCCCTGTGTGGGCCCTGCTGTGTGATACCCGGACCCCT
Db	2821	GCCGGCCACCGGCTATTCCCTGTGTGGGCCCTGCTGTGTGATACCCGGACCCCT
Qy	2888	GCAGAGGCACTACTCAGCTATGCGGAGACCTCAATCAGAGCGAGTCTACCTTT
Db	2881	GCAGAGGCACTACTCAGCTATGCGGAGACCTCAATCAGAGCGAGTCTACCTTT
Qy	2948	CGGCTTCAAGGCTGGAGGAAACATGCGTCGAAACTCTTTGGGGTCTTTGGCGCT
Db	2941	CGGCTTCAAGGCTGGAGGAAACATGCGTCGAAACTCTTTGGGGTCTTTGGCGCT
Qy	3008	TCACAGCCTGTTTCGATTTTGGAGTGAAACAGCTCCAGACGGTGTGCAACAA
Db	3001	TCACAGCCTGTTTCGATTTTGGAGTGAAACAGCTCCAGACGGTGTGCAACAA
Qy	3068	CAAGATCTCTGCTGCGAGCGTACAGGTTTCCACGCATGTGCTGCGAGCTCC
Db	3061	CAAGATCTCTGCTGCGAGCGTACAGGTTTCCACGCATGTGCTGCGAGCTCC
Qy	3128	TCAGCAGTTTGGAGAACCCCAATTTTCTCGCGCTCATCTGTGACAGGCT
Db	3121	TCAGCAGTTTGGAGAACCCCAATTTTCTCGCGCTCATCTGTGACAGGCT
Qy	3188	CTGCTACTCCATCTGAAAGCCAGAACGCGAGGATGTGCTGGGGGCCAAGGG
Db	3181	CTGCTACTCCATCTGAAAGCCAGAACGCGAGGATGTGCTGGGGGCCAAGGG
Qy	3248	CGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCAACCAAGCATTTCTGCT
Db	3241	CGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCAACCAAGCATTTCTGCT
Qy	3308	GACTCGACACGTTGTCACTAGTGGCACTCTCTGGGGTCACTCAGAGCAGGCCAC
Db	3301	GACTCGACACGTTGTCACTAGTGGCACTCTCTGGGGTCACTCAGAGCAGGCCAC
Qy	3368	GCTGAGTCGGAAGCTCCCGGGAGACAGCTGACTGCCCTGGAGGCCGAGAGCCAA
Db	3361	GCTGAGTCGGAAGCTCCCGGGAGACAGCTGACTGCCCTGGAGGCCGAGAGCCAA
Qy	3428	ACTGCCCTCAGATTCAGAGCAATCCTTGGACTGATGCGCCACCCGCCCAAGCCAC
Db	3421	ACTGCCCTCAGATTCAGAGCAATCCTTGGACTGATGCGCCACCCGCCCAAGCCAC
Qy	3488	GAGCAGACACGAGACCTCTGTCAGCGCGGCTCTACGTCCAGAGGAGGAGGGG
Db	3481	GAGCAGACACGAGACCTCTGTCAGCGCGGCTCTACGTCCAGAGGAGGAGGGG
Qy	3548	CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCGCTGAGTGAATTTTGGCCGAC

E/KEY: CDS

E/KEY: CD3
ATTENTION: 561..3454

ER INFORMATION: /product= "human telomerase reverse

nsriptase (hTRT)"

DESCRIPTION: SEQ ID NO: 1;

99.3%; Score 4015; DB 9; Length 4015;
 larity 100.0%; Pred. No. 0;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

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3CTGGCCACGTTCTGGTGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGACGCCGG 187

3CTGGCCACGTTCTGTGGGGCCCTGGGGCCCAAGGCTGGGCTGGTGCAGCGCG 180

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CCCGCGGCTTCCGCGCGTGGTGGCCAGTGCCCTGGTGTGGTGCCCTGGGACGC 240

[illegible]

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3CTGGA CGGGCC CGCGGGGCCCCCGAGGCCCTTCACCA CAGCGTGCGCAGCTA 420

3CCCAACAAGGTGACCGACGCACTCGGGGGGAGCGGGGGCTGCTGCTGCC 487

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Andrews, William H.
 INVENTION: Human Telomerase Catalytic Subunit
 OF SEQUENCES: 633
 INDECE ADDRESS:
 RESSEE: Townsend and Townsend and Crew LLP
 SET: Two Embarcadero Center, Eighth Floor
 Y: San Francisco
 TE: California
 NTRY: USA
 NTRY: 94111-3834
 READABLE FORM:
 IUM TYPE: Floppy disk
 IPUTER: IBM PC compatible
 RATING SYSTEM: PC-DOS/MS-DOS
 TWARE: PatentIn Release #1.0, Version #1.30
 APPLICATION DATA:
 APPLICATION NUMBER: US/10/325,810
 ING DATE: 20-Dec-2002
 SSIFICATION: <Unknown>
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 LICATON NUMBER: US/09/402,181
 ING DATE: 29-Sep-1997
 LICATON NUMBER: US 08/724,643
 ING DATE: 01-OCT-1996
 LICATON NUMBER: US 08/844,419
 ING DATE: 18-APR-1997
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 ING DATE: 25-APR-1997
 LICATON NUMBER: US 08/851,843
 ING DATE: 06-MAY-1997
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 ING DATE: 14-AUG-1997
 LICATON NUMBER: WO PCT/US97/17885
 ING DATE: 01-OCT-1997
 AGENT INFORMATION:
 IE: Ausenhus, Scott L.
 ISTRATION NUMBER: 42,271
 ERENCE/DOCKET NUMBER: 015389-002620US
 UNICATION INFORMATION:
 EPHONE: (415) 576-0200
 EFAX: (415) 576-0300
 OR SEQ ID NO: 1:
 CHARACTERISTICS:
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 E: nucleic acid
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 OLOGY: linear
 TYPE: cDNA
 IE/KEY: CDS
 ATION: 56..3454
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 te= "human telomerase reverse
 nscriptase (hTERT) catalytic protein
 ponent"
 DESCRIPTION: SEQ ID NO: 1:

99.3%; Score 4015; DB 13; Length 4015;
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 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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TION: Embryonic Stem Cells
: DATE: 2003-03-13
ID NOS: 139
om
o sapiens
);..(3454)
TION:

US-10-388-578-1
Query Match 99.3%; Score 4015; DB 13; Length 4015;
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Matches 4015; Conservative 0; Mismatches 0; Indels 0;
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3601	Db		CATGTCCGGCTGA	GGCTGAGTGT	CCGGCTGAGG	CCTGAGC	GAGTGT	CCAGGCCAA	
3668	QY		GAGTGTCCAGCAC	ACTGCGGCTT	CATCTTCCCA	CAGGCTG	GGCGCTCGGCTCCG		
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RESULT 10

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US-10-208-243-1
; Sequence 1, Application US/10208243
; Publication No. US20030044394A1
; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.
; APPLICANT: Genon Corporation
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune Response to a Telomerase Antigen
; TITLE OF INVENTION: Response to a Telomerase Antigen
; FILE REFERENCE: 015389-003500PC
; CURRENT APPLICATION NUMBER: US/10/208,243
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US/09/675,321
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/112,006
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT)
US-10-208-243-1

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Query Match.      99.3%; Score 4015; DB 15; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4015; Conservative 0; Mismatches 0; Indels 0;

QY      8 GCAGCGGTGGTCTCTCTCGGCACGTGGGAAGCCCTGGCCCGCGGCCACCCCGCGC
DP      1 GCAGCGGTGGTCTCTCTCGGCACGTGGGAAGCCCTGGCCCGCGGCCACCCCGCGC

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3961	Db	
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RESULT 11

RESULT 11
US-10-054-295-224

US-10-054-295-224
; Sequence 224, Application US/10054295

US 20030044953A1

; PUBLICATION NO. US2003
; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

;
AFFILIANT: CECIL, THOMAS R.
;
Lingner, Joachim

; ;
Pringner, Oscar
Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin

Andrews, William H.

TITLE OF INVENTION: No. US20030044953A1el Telomerase

; TITLE OF INVENTION: NO.
; NUMBER OF SEQUENCES: 225
;

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

STREET: TWO EMBALC
CITY: San Francisco

CITY: San Francisco
STATE: California

STATE: California
COUNTRY: United States of America

COUNTRY: U
ZIP: 94111

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; ZIP: 94111
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; MEDIUM TYPE: Floppy disk
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; MEDIUM TYPE: FLOPPY disk
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS

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OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30
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APPLICATION DATA:
 PPLICATION NUMBER: US/10/054,295
 FILING DATE: 18-Jan-2002
 ASSIFICATION: 536
 APPLICATION DATA:
 PPLICATION NUMBER: 08/854,050
 FILING DATE: <Unknown>
 PPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 PPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 PPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 Y/AGENT INFORMATION:
 RE: Apple, Randolph T.
 FIRM/INVENTOR NUMBER: 36,429
 SIRENCE/DOCKET NUMBER: 015389-0029300S
 MUNICATION INFORMATION:
 LEPHONE: (415) 576-0200
 LEFAX: (415) 576-0300
 FOR SEQ ID NO: 224:
 S CHARACTERISTICS:
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 PE: nucleic acid
 RANDEDNESS: single
 POLOGY: linear
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 E/KEY: CDS
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 ote= "human telomerase reverse
 transcriptase (hTERT) catalytic protein
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99.3%;	Score	4015;	DB	15;	Length	4015;	
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Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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  RMATION:
  AT: Cech, Thomas R.
      Lingner, Joachim
      Nakamura, Toru
      Chapman, Karen B.
      Morin, Gregg B.
      Harley, Calvin
      Andrews, William H.
  F INVENTION: No. US2003005978A1el Telomerase
  OF SEQUENCES: 225
  ONDENCE ADDRESS:
  DRESSEE: Townsend and Townsend and Crew LLP
  REET: Two Embarcadero Center, 8th Floor
  TY: San Francisco
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  UNTRY: United States of America
  P: 94111
  R READABLE FORM:
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  APPLICATION DATA:
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  LING DATE: 18-Jan-2002
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  Y/AGENT INFORMATION:
  ME: Apple, Randolph T.
  GISTRATION NUMBER: 36,429
  REFERENCE/DOCKET NUMBER: 015389-002930US
  MUNICATION INFORMATION:
  LEPHONE: (415) 576-0200
  LEFAX: (415) 576-0300
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  E TYPE: CDNA
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ACTION:
ron Corporation

ron Corporation
announcing a bid to

enning, Chris

Lark, A. John

chiff, J. Michael

NTION: Transplantation and a Carbohydrate Determinant Selection System

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; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; ; Lingner, Joachim
; ; Nakamura, Toru
; ; Chapman, Karen B.
; ; Morin, Gregg B.
; ; Harley, Calvin
; ; Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DI
; ; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
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; APPLICATION NUMBER: US/10/044,692
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
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; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
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; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
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; APPLICATION NUMBER: US 08/724,643
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; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/POCKET NUMBER: 015389-0026000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
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RESULT 15

US-10-044-539-1
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GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin
 Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DI
 THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

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99.3%; Score 4015; DB 15; Length 4015;
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24: em_gsa_pro:*
25: em_gsa_rtd:*
26: em_gsa_phg:*
27: em_gsa_vrl:*
28: gb_gsl:*
29: gb_gsl2:*

is the number of results predicted by chance to have a
ter than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

Query	Length	DB	ID	Description
39.2	1826	29	AY407349	Homo sapi
32.4	1584	29	AY407350	Pan trogl
22.5	1835	29	AY407351	Mus muscu
19.9	925	12	BM453198	AGENCOURT

	5	500.2	12.4	851	13	BU702370
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	12	340.4	8.4	649	14	CF531069
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	14	317.8	7.9	664	13	BQ258274
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	16	290.8	7.2	614	10	BB651920
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	18	267	6.6	866	10	BE371943
	19	252.2	6.2	715	10	BE396925
	20	249.6	6.2	403	9	AA311750
	21	248.8	6.2	679	10	BE396606
	22	243.2	6.0	649	10	BE514070
	23	243	6.0	610	10	BE514188
	24	214	5.3	344	14	CF531258
	25	208.6	5.2	779	10	BE268183
	26	203.8	5.0	336	13	BY775178
	27	203.2	5.0	343	13	BY783093
	28	200.6	5.0	338	13	BY784804
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	30	189.2	4.7	753	13	BU452535
C	31	182.6	4.5	347	10	AW244516
	32	180.2	4.5	880	13	BU377259
	33	167.6	4.1	775	12	BI388013
	34	165	4.1	712	13	EX886589
	35	154.8	3.8	696	13	BU139751
	36	150.4	3.7	668	14	CA380121
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	38	132	3.3	641	28	AZ972318
	39	128.8	3.2	875	13	BU122597
C	40	123.8	3.1	813	12	BG198331
	41	116.8	2.9	632	14	CA353864
	42	115.8	2.9	732	13	EX889962
	43	114.8	2.8	654	13	EX882610
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	45	113.4	2.8	568	13	EX521269

ALIGNMENTS

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DEFINITION Homo sapiens TERT gene, VIRTUAL TRANSCRIPT, partial sequ
AY407349
ACCESSION AY407349
VERSION AY407349.1 GI:39763320
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Eute
Mammalia; Eutheria; Primates; Catarrhini; Hom
1 (bases 1 to 1826)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejar
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murph
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse or
gene trios
Science 302 (5652), 1960-1963 (2003)
JOURNAL
PUBMED 14671302
REFERENCE 2 (bases 1 to 1826)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejar
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murph
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.
Adams, M.D. and Cargill, M.
Direct Submission
TITLE

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Gaithersburg, MD 20850, USA
: sequence was made by sequencing genomic exons and ordering
: based on alignment.

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 mRNA sequence.

3198
 3198.1 GI:18502238

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 alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 cases 1 to 925)
 4GC http://mgc.nci.nih.gov/.
 nal Institutes of Health, Mammalian Gene Collection (MGC)
 ublished (1999)
 act: Robert Strausberg, Ph.D.
 l: cgapbs-remail.nih.gov
 ie Procurement: ATCC
 a Library Preparation: Life Technologies, Inc.
 a Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 Sequencing by: Agencourt Bioscience Corporation
 ie distribution: MGC clone distribution information can be
 i through the I.M.A.G.E. Consortium/LLNL at:
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 Average insert size 2.1 kb."

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 ACCESSION
 BU702370
 VERSION
 BU702370.1 GI:23627105
 KEYWORDS
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute.
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur.
 1 (bases 1 to 851)
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection
 TITLE

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 BU702370
 VERSION
 BU702370.1 GI:23627105
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 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute.
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur.
 1 (bases 1 to 851)
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection
 TITLE

blished (1999)
 act: Robert Strausberg, Ph.D.
 1: cgapsb-re@mail.nih.gov
 ue Procurement: Dr. Jim Lin, University of Iowa
 A Library Preparation: Dr. M. Bento Soares, University of Iowa
 A Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 Sequencing by: Dr. M. Bento Soares, University of Iowa
 ne Distribution: MGC clone distribution information can be
 d through the I.M.A.G.E. Consortium/LLNL at:
 u://image.llnl.gov
 s clone was contributed by the Brain Molecular Anatomy Project
 p)
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 Site 2: Not I; The library was constructed according
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
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 with Ecor I adaptor, digested with NotI and then cloned
 directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is CAGCCACGAC. This library was created for the University
 Iowa Brain Anatomy Project (BMAP): "Gene discovery in the
 Developing Mouse Nervous System", supported by National
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 program coordinator."

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 VERSION
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 1 (bases 1 to 468)
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 National Cancer Institute, Cancer Genome Anatomy Project
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapsb-re@mail.nih.gov
 Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael
 Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
 Technologies, Inc. cDNA Library Arrayed by: Christa Pran
 I.M.A.G.E. Consortium DNA Sequencing by: Washington Univ
 Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution informa
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 www.bio.llnl.gov/bbrp/image/image.html
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Library constructed by Life Technologies.

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 V.S., Hahn, Y., Oh, J. H., Lee, J. Y., Ahn, H. Y., Chu, M. Y., Kim, M. R.,
 J., Cheong, J. E., Sohn, H. Y., Kim, J. M., Park, H. S., Kim, S. and
 Y. S.
 Frontier Korean EST Project 2001
 clished (2002)
 act: Kim YS
 ne Research Center
 a Research Institute of Bioscience & Biotechnology
 Jeon-dong Yuseong-gu, Daejeon 305-333, South Korea
 +82-42-860-4470
 +82-42-860-4409
 1: yongsung@mail.kribb.re.kr
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ORIGIN

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 QY 2775 GTGAACCTCCCTGTAGAGACGAGGCGCTGCTGGGATACCCGGACCGCTTGTTCAGATG
 Db 1 GTGAACCTCCCTGTAGAGACGAGGCGCTGCTGGGATACCCGGACCGCTTGTTCAGATG
 QY 2835 CACGGCCTATTCCCTGTAGAGACGAGGCGCTGCTGGGATACCCGGACCGCTTGTTCAGATG
 Db 61 CACGGCCTATTCCCTGTAGAGACGAGGCGCTGCTGGGATACCCGGACCGCTTGTTCAGATG
 QY 2895 GACTACTCAGTATGCCGACCTCCATCAGAGCCAGTCTCAGCTTACCTTACCGC
 Db 121 GACTACTCAGTATGCCGACCTCCATCAGAGCCAGTCTCAGCTTACCTTACCGC
 QY 2955 AAGGCTGGAGGACATCGCTGCGAACTCTTTGGGCTTTCGCGCTGAAGTGT
 Db 181 AAGGCTGGAGGACATCGCTGCGAACTCTTTGGGCTTTCGCGCTGAAGTGT
 QY 3015 CTGTTTCTGGATTTGCAGGTGAACAGCGCTCCAGACGGTGTGCACCAACATCTTAC
 Db 241 CTGTTTCTGGATTTGCAGGTGAACAGCGCTCCAGACGGTGTGCACCAACATCTTAC
 QY 3075 CTCCTGCTGAGGCGTACAGGTTTCCAGCATGTGTGCTGAGCTCCCATTTTCA
 Db 301 CTCCTGCTGAGGCGTACAGGTTTCCAGCATGTGTGCTGAGCTCCCATTTTCA
 QY 3135 GTTGGAGAGACCCACATTTTCTGCGCGTCACTCTGACACGCGCTCCCTC
 Db 361 GTTGGAGAGACCCACATTTTCTGCGCGTCACTCTGACACGCGCTCCCTC
 QY 3195 TCCATCTCTGAAAGCCAGACGCGAG 3219
 Db 421 TCCATCTCTGAAAGCCAGACGCGAG 445

RESULT 8

BG917907
 LOCUS 851 bp mRNA linear EST
 DEFINITION 602820830F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:
 mRNA sequence.
 ACCESSION BG917907
 VERSION BG917907.1 GI:14298383
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mur
 1 (bases 1 to 851)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.

A Library Preparation: Life Technologies, Inc.
 A Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 Sequencing by: Incyte Genomics, Inc.
 ne distribution: MGC clone distribution information can be
 d through the I.M.A.G.E. Consortium/LLNL at:
 e: //image.llnl.gov
 e: LLML0903 row: k column: 08
 quality sequence stop: 753.
 Location/Qualifiers
 1. .851
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4949887"
 /sex="female, virgin"
 /tissue_type="infiltrating ductal carcinoma"
 /dev_stage="5 months"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Mamg"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigator
 providing samples: Jeffrey Green, M.D., NIH"

10.4%; Score 419; DB 12; Length 851;
 ilarity 71.9%; Pred. No. 4.4e-42;
 Conservative 0; Mismatches 215; Indels 11; Gaps 2;

GGTGGATGATTCCTGTTGGTGACACCTCAGCTCACCACCGGAAACCTTCCTCAGG 2717
 |||||
 GTGGATGACTTCTGTAGGTGACGCTCACTTGGACCAAGCAAAACCTTCCTCAGC 97
 |||||
 CCTGGTCCGAGGTGCTCCTCAGTATGCTGCTGCTGAACCTTGGGAGACAGTGGTG 2777
 |||||
 CCTGGTCCATGGCGCTTCTCAGTATGGTGTGATGATAACTTGCAGAGACAGTGGTG 157
 |||||
 CTTCCCTGTAGAGACGAGGCCCTGGGTGCGACCGCTTTTGTTCAGATGCGGCCAC 2837
 |||||
 CTTCCCTGTGGAGCCTGTGATCCCTGGGTGGTGCAGCTCCATACAGCTGCTGCTCAC 217
 |||||
 CCTATTCCCTGGTGGCGCTGCTGCTGGATACCGGACCGCTGGAGTGCAGAGCGAC 2897
 |||||
 CCTGTTTCCCTGGTGGTGGTGTGCTGGACACTCAGACTCTGGAGGTGTTCTGTGAC 277
 |||||
 CTCAGCTATGCTCCGAGCTCCATCAGAGCCAGTCTCACCTTCAACCGCGCTTCAG 2957
 |||||
 CTCAGGTTATGCCAGACCTCAATTAAGACGACCTCACCTTCAGAGTGTCTTCAAA 337
 |||||
 TGGAGGAAATGCGTGCAGAACTCTTTTGGGGTCTTGGCGCTGAAGTGTACAGCCTG 3017
 |||||
 TGGAGAACCATGCGGAACAAGCTCTCTGCTGGTCTTGGCGTTGAAGTGTACAGCTA 397
 |||||
 TCTGGATTTCCAGGTGAACGCTCCAGAGGTGTGCACCAACATCTACAGATCCTC 3077
 |||||
 TTAGACTTCAGGTGAACAGCTCCAGACAGTCTGCATCAATATATACAAGATCTTC 457
 |||||
 CTCGAGGCGGTACAGGTTTCCAGCATGTGTGCTGCAGCTCCCATTTTCATCAGCAAGT 3137
 |||||
 CTCCTCAGGCTCAGAGTTCCATGATGTGTGATTCAGCTTCCCTTTTGAACAGGCTGT 517
 |||||
 TAGAAGCCCAATTTTCTCGCGGTATCTCTGAACGCGCTCCCTCTGTCTACTCC 3197
 |||||
 TAGAAGCTCAGATTTCTTCTGGGCATCACTCCAGCCAGCATCTCTGCTGTATGCT 577
 |||||
 CCTGAAGCCCAAGAACGACGAGTGTGCTGGGGGCAAGGCGCGCGCCGCTCTG 3257
 |||||
 CTGAAGTCAAGAAATCCAGGAATGACATAAAGGCTCTGGCTC-----CTT 627
 |||||
 CTCGAGGCGGTGAGTGGCTGTGCCACCAAGCATTCCT-GCTCAAGCTGACTCGACA 3316
 |||||
 TCTGAGAGCCGACATTTGGTCTGTCTACAGGCTTCTCTGGCTCAAGCTGGTGTCTCA 687

QY 3317 CGGTGTACCTACGTGGCCACTCCTGGGGTCACTCAGGACAGCCAGCGACGT
 |||||
 Db 698 TTCGTGATCATCAAAATGTCTCTGGGACCTCTGAGGACAGCCCAAAACCGCT
 |||||
 QY 3377 GAAGTCCCGGGACGACGCTGACTGCCCTGGAGCGCGCAGCCAAACCGGCACT
 |||||
 Db 748 GAAGTCTCGAGAGGCGCAATGACCATGCTTACAGCTGCGAGCTGACCCAGACCT
 |||||
 QY 3437 AGACTTCAAGACCATCTCTGGACTGA 3461
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 Db 808 AGACTTTCAGGACCATTTGGACTAA 832
 |||||

RESULT 9
 AW276315/416 bp mRNA linear EST
 LOCUS X10B12.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2
 DEFINITION mRNA sequence.
 ACCESSION AW276315
 VERSION AW276315.1 GI:6663345
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom
 1 (bases 1 to 416)
 NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Chris Moshaluk, M.D., Ph.D., Michael
 Emert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
 Technologies, Inc. cDNA Library Arrayed by: Christa Pran
 I.M.A.G.E. Consortium DNA Sequencing by: Washington Univ
 Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution informa
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -400P from Glibco
 High quality sequence stop: 413.
 Location/Qualifiers
 1. 416
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2759711"
 /tissue_type="two pooled squamous cell carcinom
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_Lu28"
 /note="Organ: lung; Vector: pCMV-SPORT6; Site 1
 Site 2: NotI; Cloned unidirectionally. Primer:
 Library constructed by Life Technologies."

FEATURES
 source

ORIGIN
 Query Match 10.3%; Score 416; DB 10; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1.2e-41;
 Matches 416; Conservative 0; Mismatches 0; Indels 0;

QY 3601 AGGCTGCTGATCTCCGGCTGAAGGCTGAGTGTCTCCGGCTGAGGCTGAGCGAGTGT
 |||||
 Db 416 AGGCTGCTGATCTCCGGCTGAAGGCTGAGTGTCTCCGGCTGAGGCTGAGCGAGTGT
 |||||
 QY 3661 AAGGCTGAGTGTCTCCAGACACCTGCGCTTCTTCACTTCCCAACAGGCTGGCGCT
 |||||
 Db 356 AAGGCTGAGTGTCTCCAGACACCTGCGCTTCTTCACTTCCCAACAGGCTGGCGCT
 |||||
 QY 3721 CACCCAGGCGCAGCTTTTCTCACCAGGAGCGCGCTTCCACTCCCAACATAG
 |||||
 Db 296 CACCCAGGCGCAGCTTTTCTCACCAGGAGCGCGCTTCCACTCCCAACATAG

ATCCCCAGATTGCGCATTTGTTTACCCCTCGCCCTGCTTCTTGGCTTCCACCC 3840
 ATCCCCAGATTGCGCATTTGTTTACCCCTCGCCCTGCTTCTTGGCTTCCACCC 177
 ATCCAGGTGGAGACCTGAGAGAGCCCTGGAGCTCTGGGAATTTGGAGTGACAA 3900
 ATCCAGGTGGAGACCTGAGAGAGCCCTGGAGCTCTGGGAATTTGGAGTGACAA 117
 TGTGCCCTGTACACAGGCGAGACCCCTGATGGGGTCCCTGTGGGTCAA 3960
 TGTGCCCTGTACACAGGCGAGACCCCTGATGGGGTCCCTGTGGGTCAA 57
 TGTGCCCTGTACACAGGCGAGACCCCTGATGGGGTCCCTGTGGGTCAA 4016
 TGTGCCCTGTACACAGGCGAGACCCCTGATGGGGTCCCTGTGGGTCAA 1

296 02.r1 NCI_CGAP_GCB1 389 bp mRNA linear EST 14-AUG-1997
 sequence. IMAGE:712562 5',
 296
 296.1 GI:1924194

sapiens (human)
 sapiens
 yota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 lia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 ases 1 to 389)
 GAP http://www.ncbi.nlm.nih.gov/ncicgap.
 nal Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Gene Index
 lished (1997)
 ct: Robert Strausberg, Ph.D.
 : cgapbs-remail.nih.gov
 clone is available royalty-free through LLNL ; contact the
 Consortium (info@image.llnl.gov) for further information.
 t Length: 2187 Std Error: 0.00
 rimer: -28ml3 rev2 ET from Amersham
 quality sequence stop: 385.
 Location/Qualifiers
 1. 389
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:712562"
 /tissue_type="germinal center B cell"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP GCB1"
 /note="vector: p7T3D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was prepared from human tonsillar cells enriched for
 germinal center B cells by flow sorting (CD20+, IgD+),
 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
 (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
 primed with a Not I - oligo(dT) primer
 [5'-TGTTACCAATCTGAGTGGAGCGCGCTCATTTTTTTTTTTT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors
 and Eco RI sites of the modified p7T3 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

9.5%; Score 385.8; DB 9; Length 389;
 larity 99.5%; Pred. No. 6.4e-38;
 Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 AAGTTCTGCACTGCGTATGAGTGTGACGTCTCGAGCTGCTCAGTCTTTCTTT 1745
 AAGTTCTGCACTGCGTATGAGTGTGACGTCTCGAGCTGCTCAGTCTTTCTTT 60

1746 TATGTCACGAGACACGTTTCAAAAGAACAGAGCTCTTTTCTACCGAAGAGT
 Db 61 TATGTCACGAGACACGTTTCAAAAGAACAGAGCTCTTTTCTACCGAAGAGT
 Qy 1806 AGCAAGTTGCAAGACATTGGAATCAGACAGACACTTGAAGAGGGTGCAGCTGCGG
 Db 121 AGCAAGTTGCAAGACATTGGAATCAGACAGACACTTGAAGAGGGTGCAGCTGCGG
 Qy 1866 TCGGAGCAGAGTTCAGGAGCATCGGGAAGCCAGGCCCGCTGCTGAGCTCC
 Db 181 TCGGAGCAGAGTTCAGGAGCATCGGGAAGCCAGGCCCGCTGCTGAGCTCC
 Qy 1926 CGCTTCATCCCCAAGCCTGACGGCTCGGCCGCTGGAACATGGACTACGTC
 Db 241 CGCTTCATCCCCAAGCCTGACGGCTCGGCCGCTGGAACATGGACTACGTC
 Qy 1986 GCCAGAACGTTCCGAGAGAAAGAGGCGCGAGCGTCTACCTCGAGGGTGAAG
 Db 301 GCCAGAACGTTCCGAGAGAAAGAGGCGCGAGCGTCTACCTCGAGGGTGAAG
 Qy 2046 TTCAGCGTCTCACTACAGAGCGCGCGCG 2074
 Db 361 TTCAGCGTCTCACTACAGAGCGCGCGCG 389

RESULT 11
 CF531121 688 bp mRNA linear EST 1
 LOCUS
 DEFINITION
 IMAGE:30355988 5', mRNA sequence.
 CF531121
 ACCESSION
 VERSION
 CF531121.1 GI:34583085
 KEYWORDS
 EST.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muri
 NTH-MGC http://ngc.nci.nih.gov/
 1 (bases 1 to 688)
 AUTHORS
 TITLE
 National Institutes of Health, Mammalian Gene Collection
 JOURNAL
 Unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, Universit
 DNA sequencing by: Dr. M. Bento Soares, University of Io
 Clone Distribution: Distribution information can be four
 http://genome.uiowa.edu/distribution/mousefl.html
 This clone was contributed by the Brain Molecular Anaton
 (BMAP)

Seq primer: pyx-5.
 Location/Qualifiers
 1. 688
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:30355988"
 /tissue_type="whole brain"
 /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH BMAP_FY0"
 /note="Organ: Brain; Vector: pyx- Asc; Site 1: E
 Site 2: Not I; The library was constructed accor
 Bonaldo, Lennon and Soares, Genome Research, 6:7
 1996. Denatured RNA was size fractionated on a 1
 gel. First strand cDNA synthesis was primed with
 primer containing a Not I site. Double strand cD
 size selected according to mRNA size fraction, 1
 with EcoR I adaptor, digested with NotI and then
 directionally into pyx-Asc vector. The library t
 sequence located between the Not I site and the

FEATURES
 source

is AGCAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

8.6%; Score 346.2; DB 14; Length 688;
 ilarity 73.9%; Pred. No. 3.9e-33;
 Conservative 0; Mismatches 155; Indels 0; Gaps 0;
 XGGCCACCCCGCGATGCGCGGCTCCCGCTGCCGAGCGGTGCTCCTCTGTGG 106
 |||||
 XGGCCCTTGAACATGACCCCGGCTCTGCTGCGCGGTGCTGCTCTGTCTGCG 122
 |||||
 XCCACTACCGGAGGTGCTGCGCTGGCCAGTTCGTGCGGCGCTGCGGCCCGCAGGG 166
 |||||
 GCCGATACCGGAGGTGCGCGCTGGCAACTTGTGCGGCGCTGCGGCCCGCAGGG 192
 |||||
 GCGGCTGTGACGCGCGGACCGCGGCTTTCCGCGCGCTGCTGTCGCCAGTGCCT 226
 |||||
 GCGGCTTGTCAACCCCGGACCGCAAGATCTACCGCACTTGTGTCGCCAATGCCT 242
 |||||
 TGTGCTGCTGGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 286
 |||||
 TGTGATCACTGGGCTCAAGCGCTCCACCTGCGGACCTTTCCTTCCACAGGTGC 302
 |||||
 GCCTGAAGAGCTGTGTCGCCAGTGTGTCAGAGGCTGTGCGAGCGCGCGCGCGAGAA 346
 |||||
 CCCTGAAGAGCTGTGTCGCCAGGTTGTGTCAGAGACTGTGCGAGGCAACAGAGAA 362
 |||||
 TGCTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 406
 |||||
 TGCTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTT 422
 |||||
 CCACAGCTGCGAGCTACCTGCCACACGCTGACCGACGCTGCGGCGCGCGCGCG 466
 |||||
 CTAGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 482
 |||||
 CGTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 526
 |||||
 CATGATGCTACTGCTGAGCGAGTGGCGAGACCTGCTGCTGCTGCTGCTGCTGCTG 542
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 GCGGCTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 586
 |||||
 GTGCTCTTATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
 |||||
 ACCAGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 639
 |||||
 CTAAACCCCTCATCTTACTCAGCAGCTTCCAGCCTTAACCTTGAAGTGGGCGC 655
 |||||

1069 649 bp mRNA linear EST 12-SEP-2003
 -FY0-csp-c-19-0-UI-r1 NIH_BMAP_FY0 Mus musculus cDNA clone
 E:30355746 5', mRNA sequence.
 1069

1069.1 GI:34583033

musculus (house mouse)

musculus

Iyoda; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 alia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 bases 1 to 649)

MGC <http://mgi.ncl.nih.gov/>

onal Institutes of Health, Mammalian Gene Collection (MGC)

blished (1999)

act: Robert Strausberg, Ph.D.

1: cga@rs-mail.nih.gov

ue Procurement: Dr. Jim Lin, University of Iowa

A Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of
 Clone Distribution: Distribution information can be fo
<http://genome.uiowa.edu/distribution/mousefl.html>
 This clone was contributed by the Brain Molecular Anat
 (BMAP)

Seq primer: pYX-5.

FEATURES

Location/Qualifiers

1..649
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:30355746"
 /tissue_type="whole brain"
 /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
 /lab_host="DH10B (11 phage resistant)"
 /clone_lib="NIH_BMAP_FY0"
 /note="Organ: Brain; Vector: pYX-Asc; Site:1;
 Site 2: Not 1; The library was constructed acc
 Bernaldo, Lennon and Soares, Genome Research, 6:
 1996. Denatured RNA was size fractionated on a
 gel. First strand cDNA synthesis was primed wit
 primer containing a Not I site. Double strand c
 size selected according to mRNA size fraction,
 with EcoR I adaptor, digested with NotI and the
 directionally into pYX-Asc vector. The library
 sequence located between the Not I site and the
 is AGCAGACAG. This library was created for the
 Iowa Brain Anatomy Project (BMAP): 'Gene Discov
 Developing Mouse Nervous System', supported by
 Institute of Mental Health (NIMH), Hemin Chin,
 program coordinator."

ORIGIN

Query Match 8.4%; Score 340.4; DB 14; Length 649;
 Best Local Similarity 77.3%; Pred. No. 2e-32;
 Matches 413; Conservative 0; Mismatches 121; Indels 0;
 QY 47 CCCGCCACCCCGCGATGCGCGCGCTCCCGCTGCCGAGCGCGCTCCCT 111
 |||||
 Db 26 CCCGCCCTTGAACAATGACCCCGCGCTCCTGTTGCCCGCGGTGCGCTCTCT 111
 |||||
 QY 107 CAGCCACTACCGCAGGTGCTGCCCTGCCACAGTTCTGTCGCGCGCTGGGGCC 111
 |||||
 Db 86 CAGCCGATACCGGAGGTGTGCCCGCTGCCAACCTTTGTGCGCGCTGGGGCC 111
 |||||
 QY 167 CTGGCGGCTGTGTCAGCGCGGGGACCCCGCGGCTTTCCGCGCGCTGGTGGCCCA 111
 |||||
 Db 146 CAGGCGGCTTGTGCAACCCCGGGGACCCGAAGATCTACCGCACTTTGGTTGCCCA 111
 |||||
 QY 227 GGTGTGCTGCCCTGGGACGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 111
 |||||
 Db 206 AGTGTGATGACTGTGGGCTCACAGCTCCACCTGCCACCTTTCTTCCACCA 111
 |||||
 QY 287 CTGCTGAAGAGCTGTGTGGCCCGAGTCTGCAGAGGCTGTGCGAGCGCGCGCG 111
 |||||
 Db 266 ATCCCTGAAGAGCTGTGTGGCCAGGTTGTGCAGAGACTCTGCGAGGCGCAACA 111
 |||||
 QY 347 GGTGTGCGCTTCCGCTTCCGCTGCTGAGACGGGCGCGCGCGCGCGCGCGCGCG 111
 |||||
 Db 326 GGTGTGCGCTTCCGCTTCCGCTGCTGAGTCTTAAAGAGGCGAGGCGCGCGCGCTCCCAT 111
 |||||
 QY 407 CACACACGCTGCGCAGCTACCTGCCCAACACACAGCTGACCGACGACCTGCGGGG 111
 |||||
 Db 386 CACTAGTAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 111
 |||||
 QY 467 GGCCTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 111
 |||||
 Db 446 TGCATGATGCTACTGTTGACCGAGTGGGCGACGACCTGCTGCTGCTGCTGCTGCT 111
 |||||
 QY 527 CTGCGCGCTCTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 111
 |||||
 Db 506 CTGTGCTCTTTATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 111
 |||||

act: Robert Strausberg, Ph.D.
 l: cgapbs-remail.nih.gov
 Library Preparation: J. Baker (Stanford University)
 A Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
 Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NIHSC)
 ne distribution: NCI-CGAP clone distribution information can be
 d through the I.M.A.G.E. Consortium/LLNL at:
 @image.llnl.gov
 :1845958
 e: LLAM12043 row: N column: 7
 primer: Sp6 primer:
 Location/Qualifiers
 1. .664
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CD-1"
 /db_xref="taxon:10090"
 /clone="IMAGE:9409222"
 /dev_stage="embryo, late gastrula"
 /tissue_type="embryo, 7.5 dpc"
 /lab_host="XL1-Blue"
 /clone_lib="Baker mouse embryo e7.5"
 /note="Vector: pCS105; Site_1: NotI; Site_2: SalI; cDNA
 made by oligo-dr priming. Directionally cloned into
 SalI/NotI sites using the following 5' adaptor:
 5'-TCGACCCACGCGTCCG-3'. Size-selected for average insert
 size 1.8-1.9 kb. Library constructed by J. Baker (Stanford
 University)."

7.9%; Score 317.8; DB 13; Length 664;
 ilarity 68.3%; Pred. No. 1.2e-29;
 Conservative 0; Mismatches 177; Indels 45; Gaps 1;
 CCAGCTGACTGGCGTCCGAGCTCGTGAGACCACTTTCTGGGTTCAGGCCCTG 1174
 TTAATTTGACTGGGCCAGGAGACTGGTGAGATCATCTTCTGGGCTCAAGGCCCTAG 68
 TGCAGGACTCCCGCAGGTTGCCCGCTGCCCGCCAGCGCTACTGGCAATCGGCC 1234
 TATCAGGACCACTCTGCAGGACACCGCTCTATCGGTGATATCGCAGATCGGCC 128
 TGTTCGAGCTGCTTGGGAACACCGCGAGTGGCCCTACGGGGTCTCTCAAGAC 1294
 TGTTCACAGCTGCTGTGTAACCATGCAGATGCCAATATGTACAGACTCTCAGGTC 188
 ACTGCCGCTGCGAGTGGCTCACCCAGCAGCGGTGCTGTGCGCGGAGAGCC 1354
 ATTGCAGTTTCGACAGCAACCAACAGGTGACAGTGCT----- 232
 AGGGCTCTGTGGCGGCCCGAGGAGGACACAGACCCCGCTGCGTGGTGCAGCT 1414
 TCGCCAGACACAGACGCCCTGCGAGTGTACGGTCTGTGCGGGCTGCTCGCGCG 1474
 TCGGCTGACAGAGTCCCTGCGAGTATATGTTTCTTCTCGGGCTGTCTCTGCAA 323
 TGTGTGCCCCCAGCGCTCTGGGGCTCCAGGCACAAACGCGCTTCTCAGGAACAC 1534
 TGTGTCTGTAGTCTCTGGGTACAGGCACAAATGAGCGCCCTCTTTTAAAGATT 383
 AGAAGTTTATCTCGTTGGGGAATACGCGAAGCTATCACTGCAGGAAGTGTGGA 443
 TGAAGTGTGGGACTGGCTTGGCTGGCAGGAGCCAGGGGTGTGGTGTCCGGC 1654
 TGAAGTAGAGGATTTGCCACTGGCTCCGAGCAGCCCGAGGAGGAGCCGTGTCCCGC 503
 TGAAGCAGCTGCTGCGTGGAGAGATCTGCGCAAGTTCTGCACTGCGTGTGAGTGT 1714

Db 504 TGCAGAGCACCGTCTGAGGAGAGGATCCTGGCTACGTTCTGTGTTCTGGCTGAT
 QY 1715 GTACGTCTGAGCTGCTCAGTCTTCTTTTATGTCACGGAGACCGTTTCA
 Db 564 ATACGTGTGAGCTGCTTGGTCACTTTTACATCACAGAGACATTCCTCA
 QY 1775 CAGGCTCTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGC 1815
 Db 624 CAGGCTCTTTTCTACCGTAAGAGTGTGTGGAGCAAGCTGC 664

RESULT 15
 AA811084/c
 LOCUS
 DEFINITION oab5c05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1
 mRNA sequence.
 ACCESSION AA811084
 VERSION AA811084.1 GI:2880695
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom
 1 (Bases 1 to 340)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David
 Ph.D., Gerald Marti, M.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fa
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequenc
 Clone distribution: NCI-CGAP clone distribution informa
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
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 Seq primer: -40m13 fwd ET from Amersham
 High quality sequence stop: 331.
 Location/Qualifiers
 1. .340
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1319048"
 /tissue_type="germinal center B cell"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP GCB1"
 /note="Vector: p7T3D-Pac (Pharmacia) with a moi
 polylinker; Site_1: Not I; Site_2: Eco RI; let
 was prepared from human tonsillar cells enrich
 germinal center B cells by flow sorting (CD20+,
 provided by Dr. Louis M. Staudt (NCI), Dr. Davi
 (NCI) and Dr. Gerald Marti (CBER). cDNA synthe
 primed with a Not I - oligo(dT) primer
 [5'-TGTTACCAATCTGAAGTGGAGCGCGCTCATTTT
]. Double-stranded cDNA was ligated to Eco RI at
 (Pharmacia), digested with Not I and cloned into
 and Eco RI sites of the modified p7T3 vector. I
 went through one round of normalization, and wa
 constructed by Bento Soares and M. Fatima Bonal

FEATURES
 source
 1. .340
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1319048"
 /tissue_type="germinal center B cell"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP GCB1"
 /note="Vector: p7T3D-Pac (Pharmacia) with a moi
 polylinker; Site_1: Not I; Site_2: Eco RI; let
 was prepared from human tonsillar cells enrich
 germinal center B cells by flow sorting (CD20+,
 provided by Dr. Louis M. Staudt (NCI), Dr. Davi
 (NCI) and Dr. Gerald Marti (CBER). cDNA synthe
 primed with a Not I - oligo(dT) primer
 [5'-TGTTACCAATCTGAAGTGGAGCGCGCTCATTTT
]. Double-stranded cDNA was ligated to Eco RI at
 (Pharmacia), digested with Not I and cloned into
 and Eco RI sites of the modified p7T3 vector. I
 went through one round of normalization, and wa
 constructed by Bento Soares and M. Fatima Bonal

Query Match 7.8%; Score 316.4; DB 9; Length 340;
 Best Local Similarity 99.1%; Pred. No. 2.1e-29;
 Matches 339; Conservative 0; Mismatches 1; Indels 2;
 QY 3692 TCACCTCCCCACAGGCTCGGCTCCAGCCCGAGGCGCAGCTTTTCCTCAC
 Db 340 TCACCTCCCCACAGG-TGGGCTCGGCTCCAGCCCGAGGCGCAGCTTTTCCTCAC

11:43:36 2004

us-09-424-686f-1.rst

GGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATTCCGCAATTCGCAATTCGTCACCCCT 3811
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TATATGAGTTTTTTCAGTTTTTCAAAAAA 4033
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April 21, 2004, 23:41:35
ecs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

ein search, using sw model

pril 21, 2004, 16:45:51 ; Search time 88 Seconds
(without alignments)

3634.588 Million cell updates/sec

S-09-424-686F-2

961

MPAPRCRAVRLSHRYRE.....TALEAANPALSPDFKTYLD 1132

LOSUM62

apop 10.0 , Gapext 0.5

586107 seqs, 282547505 residues

its satisfying chosen parameters: 1586107

ngth: 0

ngth: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

A_Geneseq_29Jan04.*
: Geneseqp1980s.*
: Geneseqp1990s.*
: Geneseqp2000s.*
: Geneseqp2001s.*
: Geneseqp2002s.*
: Geneseqp2003as.*
: Geneseqp2003bs.*
: Geneseqp2004s.*

s the number of results predicted by chance to have a
er than or equal to the score of the result being printed,
ved by analysis of the total score distribution.

SUMMARIES

%	atch	Length	DB	ID	Description
00.0	1132	2	AAW46957	AAW46957	Human tel
00.0	1132	2	AAW90251	AAW90251	Human cat
00.0	1132	2	AAW28881	AAW28881	Human tel
00.0	1132	2	AAW32090	AAW32090	Human tel
00.0	1132	2	AAW43621	AAW43621	A human t
00.0	1132	2	AAW26580	AAW26580	Human tel
00.0	1132	4	AAW64329	AAW64329	Heart mus
00.0	1132	4	AAW99930	AAW99930	Human pro
00.0	1132	4	AAW82765	AAW82765	Human tel
00.0	1132	5	AAW29226	AAW29226	Human tel
00.0	1132	5	AAW72735	AAW72735	Human tel
00.0	1132	6	AAW42063	AAW42063	Human tel
00.0	1132	6	AAW56676	AAW56676	Human tel
00.0	1132	6	AAW58045	AAW58045	Human tel
00.0	1132	7	AAW21420	AAW21420	Human TER
00.0	1154	2	AAW61350	AAW61350	Human tel
00.0	1189	2	AAW47008	AAW47008	Glutathio
99.9	1285	2	AAW47000	AAW47000	HIS tagge
99.9	1132	2	AAW71376	AAW71376	Human tel
99.9	1132	2	AAW00627	AAW00627	Human tel
99.9	1132	2	AAW00638	AAW00638	Human tel
99.9	1132	2	AAW28401	AAW28401	Human EST
99.9	1132	3	AAW96566	AAW96566	hEST2, a

26	5954	99.9	1132	7	ADC47061
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28	5952	99.8	1132	2	AAW56113
29	5927	99.4	1166	2	AAW00647
30	5918	99.3	1405	2	AAW56101
31	5911.5	99.2	1199	2	AAW47007
32	5882	98.7	1120	2	AAW00641
33	5873	98.5	1120	2	AAW00650
34	5721	96.0	1150	2	AAW47006
35	5555	93.2	1053	2	AAW00640
36	5516	92.5	1093	2	AAW00649
37	5467	91.7	1041	2	AAW00652
38	5467	91.7	1041	2	AAW00643
39	5008	84.0	948	2	AAW00639
40	5004	83.9	948	2	AAW00648
41	4932	82.7	936	2	AAW00642
42	4923	82.6	936	2	AAW00651
43	4900	82.2	949	2	AAW61349
44	4052	68.0	807	2	AAW46997
45	4052	68.0	807	2	AAW00637

ALIGNMENTS

RESULT 1

ID	AAW46957	standard; protein; 1132 AA.
XX	AC	AAW46957;
XX	DT	13-AUG-1998 (first entry)
XX	DE	Human telomerase reverse transcriptase.
XX	KW	Human; telomerase reverse transcriptase; hTERT; TERT; diagnosis; I
XX	KW	cell proliferation; cancer; ageing; ribonucleoprotein.
XX	OS	Homo sapiens.
XX	PN	GB2317891-A.
XX	PD	08-APR-1998.
XX	PF	01-OCT-1997; 97GB-00020890.
XX	PR	01-OCT-1996; 96US-00724643.
XX	PR	18-APR-1997; 97US-00844419.
XX	PR	25-APR-1997; 97US-00846017.
XX	PR	06-MAY-1997; 97US-00851843.
XX	PR	09-MAY-1997; 97US-00854050.
XX	PR	14-AUG-1997; 97US-00911312.
XX	PR	14-AUG-1997; 97US-00912951.
XX	PR	14-AUG-1997; 97US-00915503.
XX	PR	(GERO-) GERON CORP.
XX	PR	(UYTE-) UNIV TECHNOLOGY CORP.
XX	PI	Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harle
XX	PI	Andrews WH;
XX	DR	N-PSDB; AAV22379.
XX	XX	WPI; 1998-171633/16.
XX	PT	Pure and recombinant human Telomerase Reverse Transcriptase and
XX	PT	variants - are useful in the diagnosis, prognosis and treatment
XX	XX	proliferation conditions especially cancer and ageing.
XX	PS	Claim 3; Fig 17; 387pp; English.
XX	CC	The present sequence represents human telomerase reverse transcr
XX	CC	(hTERT), which is a ribonucleoprotein. The present invention also
XX	CC	describes the following methods: (A) determining whether a test

for of hTERT, by detecting the change in hTERT recombinant polynucleotide, on administration of the compound; (B) a telomerase RNA component; (C) detection of the hTERT RNA or a sample by binding a relevant probe to the sample and amplifying and correlating the presence of complex or amplification of hTERT in the sample; and (D) increasing the presence of a vertebrate cell by increasing hTERT expression; and (E) in agent that causes an increase in cell vertebrate cell in to create a medicament that inhibits ageing. A protein of hTERT and the polynucleotide encoding hTERT can be used in the of medicaments for inhibiting the effect of ageing or inhibitors of telomerase activity can be used to treat conditions associated with high telomerase activity. A protein preparation also be used in the new methods

12 AA;

100.0%; Score 5961; DB 2; Length 1132;

Clarity 100.0%; Pred. No. 0;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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APRCRAVSLRSHYREVLPATFVRLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 60

APRCRAVSLRSHYREVLPATFVRLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 120

APRCRAVSLRSHYREVLPATFVRLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 120

APRCRAVSLRSHYREVLPATFVRLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 180

APRCRAVSLRSHYREVLPATFVRLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 180

APRCRAVSLRSHYREVLPATFVRLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 240

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APRCRAVSLRSHYREVLPATFVRLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 300

APRCRAVSLRSHYREVLPATFVRLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 300

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APRCRAVSLRSHYREVLPATFVRLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 420

APRCRAVSLRSHYREVLPATFVRLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 480

APRCRAVSLRSHYREVLPATFVRLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 480

APRCRAVSLRSHYREVLPATFVRLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 540

APRCRAVSLRSHYREVLPATFVRLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 540

APRCRAVSLRSHYREVLPATFVRLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 600

APRCRAVSLRSHYREVLPATFVRLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 600

APRCRAVSLRSHYREVLPATFVRLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 660

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APRCRAVSLRSHYREVLPATFVRLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 720

APRCRAVSLRSHYREVLPATFVRLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 720

APRCRAVSLRSHYREVLPATFVRLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 780

APRCRAVSLRSHYREVLPATFVRLGPGQWRLVQRGDPAAFRALVAQCLVCVPM 780

Db 721 PQDLRLTEVIASIIKPNQTYCVRVAVVQKAAHGHVRKAFKSHVSTLTLDLPYMR

Qy 781 QETSPDLDAVIVIEOSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCQGIPOG

Db 781 QETSPDLDAVIVIEOSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCQGIPOG

Qy 841 LCSLCYGDGMENKLPAGIRRDGGLLRLLVDDFLVTPHPLTHAKTFLRLTLVRGVPEY

Db 841 LCSLCYGDGMENKLPAGIRRDGGLLRLLVDDFLVTPHPLTHAKTFLRLTLVRGVPEY

Qy 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEQSDYSYARTSI

Db 901 RKTVVNPFVEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEQSDYSYARTSI

Qy 961 NRGFKAGNRWRKLPGLVRLKCHSLFLDLQVNSLQTVCTNIIYKILLQAVRFHA

Db 961 NRGFKAGNRWRKLPGLVRLKCHSLFLDLQVNSLQTVCTNIIYKILLQAVRFHA

Qy 1021 FHQVQWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCI

Db 1021 FHQVQWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCI

Qy 1081 KLTHRVTVYVPLLGSLRTAQQLSRKLPFGTTLTALAAANPALPSDFKTIILD 1

Db 1081 KLTHRVTVYVPLLGSLRTAQQLSRKLPFGTTLTALAAANPALPSDFKTIILD 1

RESULT 2

AAW90251

ID AAW90251 standard; protein; 1132 AA.

XX AC AAW90251;

XX DT 24-MAY-1999 (first entry)

XX DE Human catalytic telomerase sub-unit protein.

XX KW Human; catalytic telomerase subunit; therapy; diagnosis; htc; a; modulator; treatment; inhibit; cellular disorder; death; defect; ageing; antisense; neoplastic cell; telomerase-related condition; tumour cell.

XX OS Homo sapiens.

XX PN WO9859040-A2.

XX PD 30-DEC-1998.

XX PF 09-JUN-1998; 98WO-EP003468.

XX PR 20-JUN-1997; 97DE-01026329.

XX PR 26-MAR-1998; 98DE-01013274.

XX PR 14-APR-1998; 98DE-01016496.

XX PA (FARB) BAYER AG.

XX PI Hagen G, Siegmund H, Weichel W, Wick M, Zubov D;

XX DR WPI; 1999-081276/07.

XX DR N-PSDB; AAV72117.

XX PT New catalytically active subunit of human telomerase - used in modulation of telomerase activity, particularly for treating ageing.

XX PS Claim 2; Fig 2; 76pp; German.

XX CC This sequence represents a novel human catalytic telomerase subunit (hTERT). This protein can be used in screening assays to identify modulators of telomerase and to treat or inhibit cellular disorder, death, defects and/or other pathological processes involving telomerase, particularly cancer and ageing (also suitable for this agent to stimulate, inhibit or mimic the activity of the subunit). Antisense

s inhibit telomerase action (by binding to specific mRNA), in neoplastic cells and may be expressed in vivo. Antibodies of the protein, used as probes or primers, are used to omerase-related conditions (especially neoplasia) by (i) normal levels of the subunit protein in body fluids or ii) by measuring the amount of the encoding nucleic acid. f the nucleic acid encoding the subunit mRNA is confined to , in contrast to the ubiquitous expression of the telomerase

2 AA;

100.0%; Score 5961; DB 2; Length 1132;

larity 100.0%; Pred. No. 0;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

APRCRAVRSLLRSYREVLPLATFVRRLPGQWRLVORGDPAPAFRALVAQCLVCVPV 60
APRCRAVRSLLRSYREVLPLATFVRRLPGQWRLVORGDPAPAFRALVAQCLVCVPV 60

PPPAAPFRQVSCLELVARVLQBLRCRGAKNVLAFGFALLDARGGPPPEAFTTSVR 120
PPPAAPFRQVSCLELVARVLQBLRCRGAKNVLAFGFALLDARGGPPPEAFTTSVR 120

PNTVTDALRGSGANGLLRRVGGDDVLLHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180
PNTVTDALRGSGANGLLRRVGGDDVLLHLLARCALFVLVAPSCAYQVCGPPLYOLGA 180

ARPPPHASGRRRLRCERAMNHSVREAGVPLGLPAGARRRGGASRLPLPKPRR 240
ARPPPHASGRRRLRCERAMNHSVREAGVPLGLPAGARRRGGASRLPLPKPRR 240

PEPERTVQGSWAHPGRTGDRGFCVSPARPAEATSLEGALSGTRHSHPSVG 300
PEPERTVQGSWAHPGRTGDRGFCVSPARPAEATSLEGALSGTRHSHPSVG 300

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HAGPSTSRPRPMDTCCPPVYAEKTHFLYSSGDKQELRPSFLISSRLPSLTGARRL 360

IFLGSRPWMPGTPTRLPLPORYQWMPRLFLLELGNHAQCPYGVLLKTHCPLRAAVT 420
IFLGSRPWMPGTPTRLPLPORYQWMPRLFLLELGNHAQCPYGVLLKTHCPLRAAVT 420

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GVCAREXPGQSAAPAEEDTDPRLLVQLLRQHSSPQWYGVFVRACLRLVPPGLMGS 480

ERRFLRNTKKFISLGHAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540
ERRFLRNTKKFISLGHAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREEI 540

FLHLMMSVYVVELLRSPFYVTETTFQKNRFFYRKSVMSKLSQIGIRQHLKRVOLRE 600
FLHLMMSVYVVELLRSPFYVTETTFQKNRFFYRKSVMSKLSQIGIRQHLKRVOLRE 600

AEVRQHREARPAALTSRLRPIPKDGLRPIVNDYVVGARTFRREKAERLTSRVKA 660
AEVRQHREARPAALTSRLRPIPKDGLRPIVNDYVVGARTFRREKAERLTSRVKA 660

VLNVERARRPCLLGASVLGLDDTHRAWRTFVLVRADDPPELYFVKVDVTGAYDTI 720
VLNVERARRPCLLGASVLGLDDTHRAWRTFVLVRADDPPELYFVKVDVTGAYDTI 720

RLTEVIASIIKQNTYCVRRVAVVQKAAGHVRKAFKSHVSTLTDLOPYMRQFVAHL 780
RLTEVIASIIKQNTYCVRRVAVVQKAAGHVRKAFKSHVSTLTDLOPYMRQFVAHL 780

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SPLRDVAVIEQSSSLNEASSGLFDVFLRFMCHAVRIRGKSYVQCQIPIQGSILSTL 840

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Db 841 LCSLCYGD MENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRLVIRGVPPEY
Qy 901 RKTVMVPPVEDEALGCTAFVQMPAHGLFPMWGLLDTTTLTLEVDSSYARTSH
Db 901 RKTVMVPPVEDEALGCTAFVQMPAHGLFPMWGLLDTTTLTLEVDSSYARTSH
Qy 961 NRGFKAGRNRRRLKFLGVRLKCHSLFLDLQVNSLQVCTNIIYKILLQAYRFHAC
Db 961 NRGFKAGRNRRRLKFLGVRLKCHSLFLDLQVNSLQVCTNIIYKILLQAYRFHAC
Qy 1021 FHQOVWKNPTFFFLRVISDTASLCYSILKAKNAGMSLGAAGAAGPLPSEAVQWLCE
Db 1021 FHQOVWKNPTFFFLRVISDTASLCYSILKAKNAGMSLGAAGAAGPLPSEAVQWLCE
Qy 1081 KLTRHRTVTVVPLLGSRRTAQTQLSRKLPGTTLTALAAANPALPSPDKTILD 11
Db 1081 KLTRHRTVTVVPLLGSRRTAQTQLSRKLPGTTLTALAAANPALPSPDKTILD 11

RESULT 3

AAV28881

ID AAV28881 standard; protein; 1132 AA.

XX AAV28881;

XX 17-JAN-2000 (first entry)

XX Human telomerase reverse transcriptase protein.

XX Human telomerase reverse transcriptase protein; hTERT; telomerase
catalytic protein component; cell proliferative capacity; DNA p;
telomerase substrate; telomeric DNA synthesis; cell immortality;
neoplastic phenotype; diagnostic application; prognostic applica
telomerase related condition; cancer; therapeutic agent;
telomerase expression; telomerase activity.

Homo sapiens.

XX

XX Key Location/Qualifiers

XX Misc-difference 608 /note= "Corresponds to cac codon"

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QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLLGPOGWRLVORGDPAAFRALVAQC:

|||||
RPPPAAPFRQVSKELVARVLQRLCERGAKNVLAFFGALLDGAAGPPPEAFITTSVR 120
RPPPAAPFRQVSKELVARVLQRLCERGAKNVLAFFGALLDGAAGPPPEAFITTSVR 120
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LPNTVTDALRGSGAWGLLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
DARPPPHASGPRRLGCRANWHSVREAGVPLGLPAPGARRGSGASRSLSPLPKRPRR 240
DARPPPHASGPRRLGCRANWHSVREAGVPLGLPAPGARRGSGASRSLSPLPKRPRR 240
APPERTFVQGGSWAHPGTRGSDRGFCVVSAPARPAEATSLGALSGTRHSHPSVG 300
APPERTFVQGGSWAHPGTRGSDRGFCVVSAPARPAEATSLGALSGTRHSHPSVG 300
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HAGPSTSPRPMPWTGPPVVAETKHFIYSSGDEQLRPSFLLSLRPSLTGARRL 360
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CIFLGRPMMPGTGPRRLPRLPQRYWQMRPLFELGNHAQCPYGVLLKTHCPRAAVT 420
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AGVAREKPGQSVAAPEEEDTDRRLVQLLRHSSPMQVYGFVRACLRRLRLLVPPGLMGS 480
VERFRANTKKFISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREI 540
VERFRANTKKFISLGHAKLSLOELTWKMSVRDCAWLRSPGVGCVPAAEHRLREI 540
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AEVROHREARPAALLTSRLRFIPKPDGLRPINMDYVVGARTFRREKRAERLTSRVA 660
AEVROHREARPAALLTSRLRFIPKPDGLRPINMDYVVGARTFRREKRAERLTSRVA 660
VNLNERARRPGLLGASVLGLDDIHRANRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
VNLNERARRPGLLGASVLGLDDIHRANRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
RLTEVIASTIKPQNTYCVRRYAVVOKAAHGHVKAFKSHVSTLTDLPYMRQFVAHL 780
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SPLRDAVVIQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSVQCGIPQGSILSTL 840
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QVWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAPLL 1080
RHRVTYVPLLSRLTAQQLSRKLPCTTTLTALEAAANPALPSPDFKTILD 1132
|||||

1081 KLTRHRTVTVYVPLLSRLTAQQLSRKLPCTTTLTALEAAANPALPSPDFKTILD 1

RESULT 5
ID AAY43621 standard; protein; 1132 AA.
XX AAY43621;
XX 26-JAN-2000 (first entry)
XX A human telomerase reverse transcriptase (TERT) polypeptide.
XX Human; telomerase reverse transcriptase; TERT; T lymphocyte acti
KW dendritic cell; telomerase activity; cancer cell; proliferating
KW immunological destruction; telomerase; cancer; proliferation di
XX Homo sapiens.
XX WO9950392-A1.
XX 07-OCT-1999.
XX 30-MAR-1999; 99WO-US006698.
XX 31-MAR-1998; 98US-0112006P.
XX (GERO-) GERON CORP.
XX Gaeta PCA;
XX WPI; 1999-610845/52.
XX N-PSDB; AAZ30154.
XX Eliciting an in vivo immune response for prevention and treatme
XX Cancers.
XX Claim 3; Fig 1; 26pp; English.
XX The present sequence represents a human telomerase reverse tran
(TERT) polypeptide. The protein is used in the method of the inv
The specification describes a method for activating a T lymphoc
comprising contacting the T lymphocyte with a dendritic cell th
expresses a TERT peptide in the context of a MHC class I or MHC
molecule. The protein causes induction of an in vivo immunologi
response to telomerase activity. Cancer cells are characterized
expression of endogenous TERT gene and the presence of detectabl
telomerase activity. Therefore, by eliciting a specific immune
to TERT or to TERT-expressing cells, it is possible to selectivel
proliferating cells for immunological destruction. The method i
eliciting an in vivo immune response to telomerase by activatin
lymphocyte, and is useful for prevention and treatment of cance
other proliferation diseases/conditions

Query Match 100.0%; Score 5961; DB 2; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;
Qy 1 MPAPRCRAVRSLLRSHYREVLPATFVRLRPGQWRLVQGDPAAPRALVAQCI
Db 1 MPAPRCRAVRSLLRSHYREVLPATFVRLRPGQWRLVQGDPAAPRALVAQCI
Qy 61 DARPPPAAPFRQVSKELVARVLQRLCERGAKNVLAFFGALLDGAAGPPPEAF
Db 61 DARPPPAAPFRQVSKELVARVLQRLCERGAKNVLAFFGALLDGAAGPPPEAF
Qy 121 SYLPTNTVTDALRGSGAWGLLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPI
Db 121 SYLPTNTVTDALRGSGAWGLLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPI
Qy 181 ATQARPPPHASGPRRLGCRANWHSVREAGVPLGLPAPGARRRGGSGASRSPLF

QARPPPHASGPRRLGGERANWHSVREAGVPLGLPAPGARRRGSGASRSPLPRPRR 240
 APERPTVPGGSAHAGRTGRGDRGFCVVSAPARPAEATSLGALSCTGRSHSPSVG 300
 APERPTVPGGSAHAGRTGRGDRGFCVVSAPARPAEATSLGALSCTGRSHSPSVG 300
 HHAGPPTSRPRPMDTPCPVYATKHFLYSSGDKQLRPSFLLSRLPSLTGARL 360
 HHAGPPTSRPRPMDTPCPVYATKHFLYSSGDKQLRPSFLLSRLPSLTGARL 360
 TIFLGSPPMDGTPRRPLPRLPQRYWQMRPLFLELLGNHACQPYGVLTAKTCHPIRAATV 420
 TIFLGSPPMDGTPRRPLPRLPQRYWQMRPLFLELLGNHACQPYGVLTAKTCHPIRAATV 420
 AGVCAREKPGQSVAAPEEDTPRRLLVQLLRQSHSPQVYGFVRACLRLRLVPPGLWS 480
 AGVCAREKPGQSVAAPEEDTPRRLLVQLLRQSHSPQVYGFVRACLRLRLVPPGLWS 480
 NERFLANTKKFISLGHAKLSLOELTWKSVRDCAWLRSPGVCVPAAEHRLREI 540
 NERFLANTKKFISLGHAKLSLOELTWKSVRDCAWLRSPGVCVPAAEHRLREI 540
 KFLHLMVSVVVELLRFFVYTTTFOKNRLFFVYKSVWMSKLSIGIROHLKVQRE 600
 KFLHLMVSVVVELLRFFVYTTTFOKNRLFFVYKSVWMSKLSIGIROHLKVQRE 600
 EAEVQREARPAALLTSRLRPIPKDGLRPIVNMVYVVGARTFRREKRAELRSVKA 660
 EAEVQREARPAALLTSRLRPIPKDGLRPIVNMVYVVGARTFRREKRAELRSVKA 660
 SVLYNEARPGLLGASVLGDDIHRAWRTFVLRAQDPPELFFVYKVDVTGAYDTI 720
 SVLYNEARPGLLGASVLGDDIHRAWRTFVLRAQDPPELFFVYKVDVTGAYDTI 720
 DRLEVIASIIKQNTYCVRYAVVQAAHGHVKAFKSHVSTLTDLPYMRQFVAHL 780
 DRLEVIASIIKQNTYCVRYAVVQAAHGHVKAFKSHVSTLTDLPYMRQFVAHL 780
 TSPURDAVITEQSSSLSNEASGGLFDVFLRFMCHHVAIRGKSVQCGIPQGSILSTL 840
 TSPURDAVITEQSSSLSNEASGGLFDVFLRFMCHHVAIRGKSVQCGIPQGSILSTL 840
 SLCYGDMENKLFAGIRRDGLLLRLVDLFLVTPLTHAKTFLRTLVRGVPEYGVVNL 900
 SLCYGDMENKLFAGIRRDGLLLRLVDLFLVTPLTHAKTFLRTLVRGVPEYGVVNL 900
 TVVNFVDEALGCTAFVQMPAHGLFPWCGLLDTTLEVSQSYSSVARTSIRASLTF 960
 TVVNFVDEALGCTAFVQMPAHGLFPWCGLLDTTLEVSQSYSSVARTSIRASLTF 960
 IFKAGRMRRKLFGLRLKCHSLFLLQVNSLQTVCTNYKILLQAYRFHACVLQLP 1020
 IFKAGRMRRKLFGLRLKCHSLFLLQVNSLQTVCTNYKILLQAYRFHACVLQLP 1020
 QWKNPTFLRVISITASI CVSILKAKNAGSLGAKGAGPLPSEAVQWLCHOAFIL 1080
 QWKNPTFLRVISITASI CVSILKAKNAGSLGAKGAGPLPSEAVQWLCHOAFIL 1080
 TRHRVTVPLLSRLTAQQLSKPLPGTTLTALAAANPALPSDFKTIID 1132
 TRHRVTVPLLSRLTAQQLSKPLPGTTLTALAAANPALPSDFKTIID 1132

undard; protein; 1132 AA.

(first entry)

ase reverse transcriptase (hTERT) enzyme.

XX Telomerase reverse transcriptase; TERT; mouse; telomere length
 KW immunogen; enzyme; telomerase-mediated DNA replication; human.
 XX Homo sapiens.
 OS WO927113-A1.
 PN 03-JUN-1999.
 XX 25-NOV-1998; 98WO-US025211.
 PR 26-NOV-1997; 97US-00979742.
 PR 16-MAR-1998; 98US-00042460.
 XX (GERO-) GERON CORP.
 PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
 XX Morin GB, Allsopp R, Depinho R, Greenberg R;
 PI WPI; 1999-347722/29.
 XX Mouse telomerase reverse transcriptase (mTERT) enzyme proteins
 PT nucleic acids.
 XX Disclosure; Fig 3; 135pp; English.
 XX The invention relates to a mouse telomerase reverse transcriptase
 CC enzyme. Compositions containing mTERT can be used in telomere l
 CC assays. Isolated mTERT is useful as an immunogen for the produc
 CC monoclonal or polyclonal antibodies. The method is useful for a
 CC the degree of purification and identification of new mTERT spec
 CC as an mTERT allele, homolog or isoform, or to screen for modula
 CC (antagonists and agonists) of telomerase-mediated DNA replicati
 CC antagonists and agonists of mTERT can be used to modify the act
 CC other telomerase enzymes such as human TERT (hTERT). The presen
 CC represents a human TERT enzyme
 SQ Sequence 1132 AA;
 Query Match 100.0%; Score 5961; DB 2; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0;
 QY 1 MPAPRCRAVRSLLRSHYREVLPLATFVRLGPOGWRVQGDPAAFALVAQC
 Db 1 MPAPRCRAVRSLLRSHYREVLPLATFVRLGPOGWRVQGDPAAFALVAQC
 QY 61 DARPPPAAPSPQVSCLELVARVLQRCERGAKNVLAFFGALLDGGAGGPEA
 Db 61 DARPPPAAPSPQVSCLELVARVLQRCERGAKNVLAFFGALLDGGAGGPEA
 QY 121 SYLNTVTDALRGSGAGLLRLRVGDDVLVHLLARCALFVLVAPSCAYQVCGPEI
 Db 121 SYLNTVTDALRGSGAGLLRLRVGDDVLVHLLARCALFVLVAPSCAYQVCGPEI
 QY 181 ATQARPPPHASGPRRLGGERANWHSVREAGVPLGLPAPGARRRGSGASRSPLJ
 Db 181 ATQARPPPHASGPRRLGGERANWHSVREAGVPLGLPAPGARRRGSGASRSPLJ
 QY 241 GAPEPERTVPGGSAHAGRTGRGDRGFCVVSAPARPAEATSLGALSCTGRH
 Db 241 GAPEPERTVPGGSAHAGRTGRGDRGFCVVSAPARPAEATSLGALSCTGRH
 QY 301 ROHHAGPPTSRPRPMDTPCPVYATKHFLYSSGDKQLRPSFLLSRLPSLT
 Db 301 ROHHAGPPTSRPRPMDTPCPVYATKHFLYSSGDKQLRPSFLLSRLPSLT
 QY 361 VETIFLGSRRPWPMDTPRRPLPRLPQRYWQMRPLFLELLGNHACQPYGVLTAKTCHPI
 Db 361 VETIFLGSRRPWPMDTPRRPLPRLPQRYWQMRPLFLELLGNHACQPYGVLTAKTCHPI
 QY 421 PAAGVCAREKPGQSVAAPEEDTPRRLLVQLLRQSHSPQVYGFVRACLRLRLVPE

GVCAREKQSGVAAPDEEDTPRLVQLRQSSSPWQVYGFVACLRRLVPPGLWGS 480
 IRRFLNTKFTISLKGKAKLSIQELTWKQSVRDCAWLRSPGVCPAAEHLREI 540
 IRRFLNTKFTISLKGKAKLSIQELTWKQSVRDCAWLRSPGVCPAAEHLREI 540
 FLHLMSSVYVVELLSFPYVTTTFOKRLFFYKSVMSKLSQSIGIRQHLKRVOLRE 600
 FLHLMSSVYVVELLSFPYVTTTFOKRLFFYKSVMSKLSQSIGIRQHLKRVOLRE 600
 AEVQHREARPAALLTSRLRFTPKDGLRPIVNDYVVGARTFRREKARLTSVKA 660
 AEVQHREARPAALLTSRLRFTPKDGLRPIVNDYVVGARTFRREKARLTSVKA 660
 VLNTERRRPGILGASVLGLDDIHRWRTFVLVRAQDPPPELVFVKVDVTGADTI 720
 VLNTERRRPGILGASVLGLDDIHRWRTFVLVRAQDPPPELVFVKVDVTGADTI 720
 RLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRAKFSHVSTLTDLPYMRQFVAHL 780
 RLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRAKFSHVSTLTDLPYMRQFVAHL 780
 SPLRDVAVIEOSSINEASSGLFVFLREMHCHAVIRGKSYVQCQIGIPQGSILSTL 840
 SPLRDVAVIEOSSINEASSGLFVFLREMHCHAVIRGKSYVQCQIGIPQGSILSTL 840
 LYGDMENKLFAGIRRDGLLRLVDDFLLVTPHLLTHAKTFLRLVGRVPEYGCVVNL 900
 LYGDMENKLFAGIRRDGLLRLVDDFLLVTPHLLTHAKTFLRLVGRVPEYGCVVNL 900
 VVNPFEDEALGTAFAVQMPAHGLFPWCGLLLDTRTLEVSQSYSSYARTSIRASLT 960
 VVNPFEDEALGTAFAVQMPAHGLFPWCGLLLDTRTLEVSQSYSSYARTSIRASLT 960
 FKAGRNMRKLFVLRKCHSLFLDLQVNSIQVCTNIYKILLQAVRPHACVQLP 1020
 FKAGRNMRKLFVLRKCHSLFLDLQVNSIQVCTNIYKILLQAVRPHACVQLP 1020
 YWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAGLPSEAVQMLCHQAFLL 1080
 YWKNPTFFLRVSDTASLCYSILKAKNAGMSLGAKGAGLPSEAVQMLCHQAFLL 1080
 YHRTVYVPLGSLRTAQTLRSKLPGLTTLTALEAANPALPSDFKTILD 1132
 YHRTVYVPLGSLRTAQTLRSKLPGLTTLTALEAANPALPSDFKTILD 1132

idard; protein; 1132 AA.

(first entry)

cell differentiation related protein SEQ ID NO: 31.

cell; human; cell differentiation; heart disease.

11.

2000WO-JP009323.

99JP-00372826.

2000WO-JP001148.

2000WO-JP007741.

HAKKO KOGYO KK.

XX Umezawa A, Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;
 PI Yamada Y;
 XX WPT; 2001-425656/45.
 DR N-PSDB; AAH48235.

XX Cells capable of differentiating into cardiomyocytes and original
 PT bone marrow or umbilical blood cells for study of cardiomyocyte
 PT differentiation and treatment of heart disease.

XX Claim 87; Page 143-147; 183pp; Japanese.

XX The present invention provides cells originating in the human bc
 CC or umbilical blood cells which are capable of differentiating in
 CC cardiomyocytes. These cells are useful in the treatment of disea
 CC involving heart muscle degeneration, such as myocardial infarcti
 CC the study of cardiomyocyte differentiation. The present sequence
 CC protein described in the exemplification of the invention

SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 4; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0;

QY 1 MPAPRCRAVRSILRSHYREVLPATFVRRLGPGQWRLVQRGDPAAFRALVAQCI
 Db 1 MPAPRCRAVRSILRSHYREVLPATFVRRLGPGQWRLVQRGDPAAFRALVAQCI
 QY 61 DARPPAPAAFRQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAF
 Db 61 DARPPAPAAFRQVSCCLKELVARVLQRLCERGAKNVLAFGFALLDARGGPPPEAF
 QY 121 SYLPTNTVTDALRGSGAWGLLLRRVGDVVLVHLARCALFVLVAPSCAYQVCGPPL
 Db 121 SYLPTNTVTDALRGSGAWGLLLRRVGDVVLVHLARCALFVLVAPSCAYQVCGPPL
 QY 181 ATQARPPPHASGPRRLGGERAWNSVREAGVPLGLPAGARRRGGSASRSLPLP
 Db 181 ATQARPPPHASGPRRLGGERAWNSVREAGVPLGLPAGARRRGGSASRSLPLP
 QY 241 GAAPERTPTVQGGWAHPGRTGRGSDRGFCVVSAPARPAEATSLGALSGRTHS
 Db 241 GAAPERTPTVQGGWAHPGRTGRGSDRGFCVVSAPARPAEATSLGALSGRTHS
 QY 301 ROHAGPSTSRPPRPMDTPCPVVAETKHFLYSSGDKQLRPSFLLSLRPSLT
 Db 301 ROHAGPSTSRPPRPMDTPCPVVAETKHFLYSSGDKQLRPSFLLSLRPSLT
 QY 361 VETIFLGRPMMPGTPRRLPRLPQRYWQMRPLFELLGNHAOCYPYVLLKTHCPL
 Db 361 VETIFLGRPMMPGTPRRLPRLPQRYWQMRPLFELLGNHAOCYPYVLLKTHCPL
 QY 421 PAAGVCAREKPGQSVAAPEEDTPRRLVQLRQSSSPWQVYGFVACLRRLVPP
 Db 421 PAAGVCAREKPGQSVAAPEEDTPRRLVQLRQSSSPWQVYGFVACLRRLVPP
 QY 481 RHNERFLNTKFTISLKGKAKLSIQELTWKQSVRDCAWLRSPGVCPAAEHLREI
 Db 481 RHNERFLNTKFTISLKGKAKLSIQELTWKQSVRDCAWLRSPGVCPAAEHLREI
 QY 541 LAKFLHLMSSVYVVELLSFPYVTTTFOKRLFFYKSVMSKLSQSIGIRQHLKRI
 Db 541 LAKFLHLMSSVYVVELLSFPYVTTTFOKRLFFYKSVMSKLSQSIGIRQHLKRI
 QY 601 LSEAEVRQHREARPAALLTSRLRFTPKDGLRPIVNDYVVGARTFRREKARLREI
 Db 601 LSEAEVRQHREARPAALLTSRLRFTPKDGLRPIVNDYVVGARTFRREKARLREI
 QY 661 LFSVINTYERARRPGLLGASVLGLDDIHRWRTFVLVRAQDPPPELVFVKVDVTG
 Db 661 LFSVINTYERARRPGLLGASVLGLDDIHRWRTFVLVRAQDPPPELVFVKVDVTG

RLTEVIASIIKQNTYCVRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
 RLTEVIASIIKQNTYCVRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQFVAHL 780
 CSPLRDVAVTEQSSSNEASSGLFDVFLRPMCHAVRIRGKSVYVQCGIQSGIISTL 840
 CSPLRDVAVTEQSSSNEASSGLFDVFLRPMCHAVRIRGKSVYVQCGIQSGIISTL 840
 ILCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRVLRGVPEYGCNVNL 900
 ILCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRVLRGVPEYGCNVNL 900
 VVNFVDEALGGTAFVQMPAHGLFPWCGLLDTLRTLEVQSDSYSSYARTSIRASLTF 960
 VVNFVDEALGGTAFVQMPAHGLFPWCGLLDTLRTLEVQSDSYSSYARTSIRASLTF 960
 IFKAGRNMRKLFGLVRLKCHSLFDLQVNSLQTVCTNTYKILLQAYRFHACVQLP 1020
 IFKAGRNMRKLFGLVRLKCHSLFDLQVNSLQTVCTNTYKILLQAYRFHACVQLP 1020
 IQVKNPTFFLRVISDTASISYILKAKNAGSLGAKGAAGPLPSEAVOWLCHQAFLL 1080
 IQVKNPTFFLRVISDTASISYILKAKNAGSLGAKGAAGPLPSEAVOWLCHQAFLL 1080
 IHRVTYVPLLSRLTAQTLGRKLPGLTTLTALEAANPALPSPDKFTILD 1132
 IHRVTYVPLLSRLTAQTLGRKLPGLTTLTALEAANPALPSPDKFTILD 1132

undard; protein; 1132 AA.

(first entry)

n #2.

; cardiant; cell differentiating agent; bone marrow;
 cell; heart disease; human.

Al.

2000WO-JP001148.

99JP-00372826.

A HAKKO KOGYO KK.

Hata J, Fukuda K, Ogawa S, Sakurada K;

8252/44.

9601.

ne marrow-originated cells capable of differentiating into
 cells, applicable as remedies for various heart diseases
 with damaged heart muscle accompanying degeneration.

Page 128-134; 158pp; Japanese.

invention relates to cells isolated from bone marrow, which
 of at least differentiating into heart muscle cells. The
 plicable as remedies for various heart diseases particularly
 heart muscle accompanying degeneration. The present sequence
 illustrate the present invention

2 AA;

Query Match 100.0%; Score 5961; DB 4; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0;
 QY 1 MPRAPCRRAVRSLLRSHYREVLPATFVRRLGPOGWRLVQKDDPAAFRALVAQC
 DB 1 MPRAPCRRAVRSLLRSHYREVLPATFVRRLGPOGWRLVQKDDPAAFRALVAQC
 QY 61 DARPPPAAPRQVSCIKELVARVLQRLCERGAKNVLAFFGALLDGGARGGPEA
 DB 61 DARPPPAAPRQVSCIKELVARVLQRLCERGAKNVLAFFGALLDGGARGGPEA
 QY 121 SYLPTNTVTDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPI
 DB 121 SYLPTNTVTDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPI
 QY 181 ATQARPPPHASGPRRLRGCEAMNHSVREAGVPLGLPAPGARRRGGSASRLPLJ
 DB 181 ATQARPPPHASGPRRLRGCEAMNHSVREAGVPLGLPAPGARRRGGSASRLPLJ
 QY 241 GAAPERTPTVQGSWAHPGRTGRGFCVVSPPAPABEATSLEGALSGRH
 DB 241 GAAPERTPTVQGSWAHPGRTGRGFCVVSPPAPABEATSLEGALSGRH
 QY 301 RQHAGGPPSTRPRPMDTPCPVYAEKHFYSSGDKQLRPSFLLSSLRPSLJ
 DB 301 RQHAGGPPSTRPRPMDTPCPVYAEKHFYSSGDKQLRPSFLLSSLRPSLJ
 QY 361 VETIFLGRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPI
 DB 361 VETIFLGRPMPGTPRRLPRLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPI
 QY 421 PAAGVCAREKPOGSVAAPBEEDTPRLVQLLRQHSSPWQYGFVRACLRLVPI
 DB 421 PAAGVCAREKPOGSVAAPBEEDTPRLVQLLRQHSSPWQYGFVRACLRLVPI
 QY 481 RHNERFLRNTKFIISLGHAKLSLQELTWKMSVRDCANLRRSPGVGCVPAAEHF
 DB 481 RHNERFLRNTKFIISLGHAKLSLQELTWKMSVRDCANLRRSPGVGCVPAAEHF
 QY 541 LAKFLHMLSVYVVELLSRFFYTTTFOKNRLLFFYRKSVMKLSQSIGIRQLKF
 DB 541 LAKFLHMLSVYVVELLSRFFYTTTFOKNRLLFFYRKSVMKLSQSIGIRQLKF
 QY 601 LSEAEVROHREARPAALLTSRLRPIKPDGLRPIVMDYVVGARTFRREKAEELI
 DB 601 LSEAEVROHREARPAALLTSRLRPIKPDGLRPIVMDYVVGARTFRREKAEELI
 QY 661 LFSVLNYERARREFGLLGASVGLGDDIHRARWTFVLRVRAQDPPPELYFVKVDVTG
 DB 661 LFSVLNYERARREFGLLGASVGLGDDIHRARWTFVLRVRAQDPPPELYFVKVDVTG
 QY 721 QDRLTEVIASIIKQNTYCVRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQ
 DB 721 QDRLTEVIASIIKQNTYCVRYAVVQKAAHGHVRKAFKSHVSTLTDLPYMRQ
 QY 781 QETSPLRDVAVTEQSSSNEASSGLFDVFLRPMCHAVRIRGKSVYVQCGIQSGI
 DB 781 QETSPLRDVAVTEQSSSNEASSGLFDVFLRPMCHAVRIRGKSVYVQCGIQSGI
 QY 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRVLRGVPEYG
 DB 841 LCSLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRVLRGVPEYG
 QY 901 RKTVMNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTLRTLEVQSDSYSSYARTSIR
 DB 901 RKTVMNPFVEDEALGGTAFVQMPAHGLFPWCGLLDTLRTLEVQSDSYSSYARTSIR
 QY 961 NRGFKAGRNMRKLFGLVRLKCHSLFDLQVNSLQTVCTNTYKILLQAYRFHAC
 DB 961 NRGFKAGRNMRKLFGLVRLKCHSLFDLQVNSLQTVCTNTYKILLQAYRFHAC

QVWKNPTFLRVISDTASLCYSLKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080
 QVWKNPTFLRVISDTASLCYSLKAKNAGMSLGAKGAGPLPSEAVQWLCHQAFLL 1080

RHRVTYVLLGSLRTAQQLSKLPGTTLTALAAANPALPSDFXTILD 1132
 RHRVTYVLLGSLRTAQQLSKLPGTTLTALAAANPALPSDFXTILD 1132

ndard; protein; 1132 AA.

(first entry)

rase protein sequence SEQ ID NO:31.

ion; heart muscle cell; cytokine; transcription factor;
 m; surface antigen; heart disease; cardiomyocyte;
 umbilical blood cell; heart muscle degeneration;
 infarction.

Al.

2000WO-JP007741.

99JP-00372826.

2000WO-JP001148.

A HAKKO KOGYO KK.

Hata J, Fukuda K, Ogawa S, Sakurada K, Gojo S;

5655/45.
 4366.

e of differentiating into cardiomyocytes and originating in
 on umbilical blood cells for study of cardiomyocyte
 ion and treatment of heart disease.

age 137-141; 187pp; Japanese.

invention describes cells originating in bone marrow or
 ood cells which are capable of differentiating into
 es. Also described are: (1) cardiomyocytes produced by the
 ion of the cells; (2) a method for carrying out the
 ion into cardiomyocytes, regulated by a promotional and/or
 actor; (3) a method for the differentiation of the cells into
 her than cardiomyocytes; (4) drug compositions promoting the
 heart muscle and regeneration of heart tissue which contain
 5) a method for the production of antibodies which recognise
 specially antibodies which recognise a surface antigen on the
 method for screening factors which promote the proliferation
 ; (7) a method for immortalising the cells by expressing
 1 them; (8) drug compositions for the treatment of heart
 i contain the immortalised cells; and (9) cell-free
 ion into cardiomyocytes. The cells are used in promoting their
 from the culture of the cells and its use in the treatment
 involving heart muscle degeneration, such as myocardial
 ad in the study of cardiomyocyte differentiation. AAH44351 to
 AAB99915 to AAB99935 represent sequences used in the
 ion of the present invention

; AA;

100.0%; Score 5961; DB 4; Length 1132;

	Best Local Similarity	100.0%;	Pred. No. 0;	Matches 1132;	Conservative	0;	Mismatches	0;	Indels	0;
QY	1	MPRAPRCRAVRSLLRSYREVLP	PLATFVRRLGPGQWRLVQRGD	PAAPALVAQC						
Db	1	MPRAPRCRAVRSLLRSYREVLP	PLATFVRRLGPGQWRLVQRGD	PAAPALVAQC						
QY	61	DARPPAAPSPROVSC	KLKELVARVLQRLCERGA	KNVLAFGFPALD	GARGGPEA					
Db	61	DARPPAAPSPROVSC	KLKELVARVLQRLCERGA	KNVLAFGFPALD	GARGGPEA					
QY	121	SYLPNTVTDALRGSG	AWGLLRVGGDVLVHLLAR	CALFVLVAPSCAYQVCGPPI						
Db	121	SYLPNTVTDALRGSG	AWGLLRVGGDVLVHLLAR	CALFVLVAPSCAYQVCGPPI						
QY	181	ATQARPPPHASGPRRL	GCERANHSVREAGVPLGL	PAPGARRRGGASASLPLI						
Db	181	ATQARPPPHASGPRRL	GCERANHSVREAGVPLGL	PAPGARRRGGASASLPLI						
QY	241	GAAPERTPVGQGSWAH	PGTRGPGSDRGFCVSP	PARPAEATLEGALSTRH						
Db	241	GAAPERTPVGQGSWAH	PGTRGPGSDRGFCVSP	PARPAEATLEGALSTRH						
QY	301	QOHAGPSTSRPRPMDT	PCPPVYATKHFLYSSG	DKQLRPSFLSSLRPSLJ						
Db	301	QOHAGPSTSRPRPMDT	PCPPVYATKHFLYSSG	DKQLRPSFLSSLRPSLJ						
QY	361	VETIFLGSRPWMEGT	PRRLPRLPQRYWQMR	PLFLELGNHAQCPYGVLLKTHCPI						
Db	361	VETIFLGSRPWMEGT	PRRLPRLPQRYWQMR	PLFLELGNHAQCPYGVLLKTHCPI						
QY	421	PAAGVCAREKPGQSV	AAPEEDTDPRRLVOLL	RQHSPPMOVYGFVRACTRLVPI						
Db	421	PAAGVCAREKPGQSV	AAPEEDTDPRRLVOLL	RQHSPPMOVYGFVRACTRLVPI						
QY	481	RHNERFLRNTKFI	SLGKHAKLSLOELTW	KMSVRDCAMLRSPGVCVPAASHF						
Db	481	RHNERFLRNTKFI	SLGKHAKLSLOELTW	KMSVRDCAMLRSPGVCVPAASHF						
QY	541	LAKFLHMLSVVYVEL	LSRFFVYTTTFOKNR	LFYRKSVWSKLQSIGIRHKLK						
Db	541	LAKFLHMLSVVYVEL	LSRFFVYTTTFOKNR	LFYRKSVWSKLQSIGIRHKLK						
QY	601	LSEAEVQRHREARPA	LLTSRLRPIPKDGLR	PVNMNDYVVGARTFREREARELT						
Db	601	LSEAEVQRHREARPA	LLTSRLRPIPKDGLR	PVNMNDYVVGARTFREREARELT						
QY	661	LFSVLNYERARRPGL	LGASVGLDDIHRAR	WTFVLRVRAQDPPPELYFVKVDVTG						
Db	661	LFSVLNYERARRPGL	LGASVGLDDIHRAR	WTFVLRVRAQDPPPELYFVKVDVTG						
QY	721	PODLRTEVIASII	KQNTYCVRYAVVQ	AAHGHVKAFAKSHVSTLTDLPYMRQ						
Db	721	PODLRTEVIASII	KQNTYCVRYAVVQ	AAHGHVKAFAKSHVSTLTDLPYMRQ						
QY	781	QETSLRDAVIEQSS	LSNEASSGLFDVFLR	FMCHAVRIRKSVYQCGIQGS						
Db	781	QETSLRDAVIEQSS	LSNEASSGLFDVFLR	FMCHAVRIRKSVYQCGIQGS						
QY	841	LCSLCYGMENKLP	AGIRDDGLLRLVDD	FLVTPHLTHAKTFLRTLVRGVEYIG						
Db	841	LCSLCYGMENKLP	AGIRDDGLLRLVDD	FLVTPHLTHAKTFLRTLVRGVEYIG						
QY	901	RKTVNFVEDEAL	CGTAFVQMPAHL	FPWCGLLDDTLTLEVQSSYSSVARTSIR						
Db	901	RKTVNFVEDEAL	CGTAFVQMPAHL	FPWCGLLDDTLTLEVQSSYSSVARTSIR						
QY	961	NRGFKAGNMRRK	LVRLKCHSLFLDL	QVNSLOTCTNLYKILLQAYRHAC						
Db	961	NRGFKAGNMRRK	LVRLKCHSLFLDL	QVNSLOTCTNLYKILLQAYRHAC						
QY	1021	FHQVWKNPTFLRVIS	DTASLCYSILKAKNAG	MSLGAKGAGPLPSEAVQWLCH						

QVWKNPTFFLRVISTASLCYSTLKAKNAGMSLGAKGAGPLPSEAVQWCHQAFLL 1080

IRHRTVTVPLIGSLRTAQOLSRKLPOTTITALEAAANPALPSDFKTILD 1132
 |||||
 IRHRTVTVPLIGSLRTAQOLSRKLPOTTITALEAAANPALPSDFKTILD 1132

andard; protein; 1132 AA.

(first entry)

rase reverse transcriptase.

reverse transcriptase; hTERT; human; cancer; tumour;
 lymphocyte; major histocompatibility complex;
 yte antigen; HLA-A2.1; vaccine.

3.

Location/Qualifiers

13..21
 /note= "HLA-A2.1 binding motif"
 23..31
 /note= "HLA-A2.1 binding motif"
 76..84
 /note= "HLA-A2.1 binding motif"
 96..104
 /note= "HLA-A2.1 binding motif"
 140..148
 /note= "HLA-A2.1 binding motif"
 152..160
 /note= "HLA-A2.1 binding motif"
 346..354
 /note= "HLA-A2.1 binding motif"
 353..361
 /note= "HLA-A2.1 binding motif"
 371..379
 /note= "HLA-A2.1 binding motif"
 388..396
 /note= "HLA-A2.1 binding motif"
 407..415
 /note= "HLA-A2.1 binding motif"
 487..495
 /note= "HLA-A2.1 binding motif"
 540..548
 /label= p540
 /note= "HLA-A2.1 binding motif"
 548..556
 /note= "HLA-A2.1 binding motif"
 555..563
 /note= "HLA-A2.1 binding motif"
 572..580
 /note= "HLA-A2.1 binding motif"
 705..713
 /note= "HLA-A2.1 binding motif"
 724..732
 /note= "HLA-A2.1 binding motif"
 772..780
 /note= "HLA-A2.1 binding motif"
 797..805
 /note= "HLA-A2.1 binding motif"
 812..820
 /note= "HLA-A2.1 binding motif"
 836..844
 /note= "HLA-A2.1 binding motif"
 863..871
 /note= "HLA-A2.1 binding motif"
 865..873
 /label= p865

/note= "HLA-A2.1 binding motif"
 883..891
 /note= "HLA-A2.1 binding motif"
 926..934
 /note= "HLA-A2.1 binding motif"
 934..942
 /note= "HLA-A2.1 binding motif"
 969..977
 /note= "HLA-A2.1 binding motif"
 988..996
 /note= "HLA-A2.1 binding motif"
 1072..1080
 /note= "HLA-A2.1 binding motif"
 1079..1087
 /note= "HLA-A2.1 binding motif"
 1095..1103
 /note= "HLA-A2.1 binding motif"
 1122..1130
 /note= "HLA-A2.1 binding motif"

WO200160391-A1.

23-AUG-2001.

15-FEB-2001; 2001WO-US005143.

15-FEB-2000; 2000US-0182685P.

15-FEB-2001; 2001US-00182685.

(REGC) UNIV CALIFORNIA.

Zanetti M;

WPI; 2001-536552/59.

Vaccine for initiating and enhancing a cytotoxic T lymphocyte re-
 sponse for treating cancers or tumors or for inducing immune response
 tumors, comprises a telomerase reverse transcriptase peptide.

Disclosure; Fig 5; 52pp; English.

The present sequence is that of human telomerase reverse transcriptase (hTERT). The sequence was analysed for 9-mer peptide sequences known binding motifs for the human leukocyte antigen HLA-A2.1 molecule. From an initial panel of about 30 candidate peptides, 2 sequences denoted p540 (see AAB82772) and p865 (see AAB82773), were examined in healthy individuals as well as patients with prostate cancer. Immunised in vitro against these 2 HLA-A2.1 restricted peptides hTERT-specific cytotoxic T lymphocytes (CTL). The cancer patients specifically lysed a variety of HLA-A2+ cancer cell lines such as prostate, breast, colon, lung and melanoma, demonstrating immune recognition of endogenously-processed hTERT peptides. In vivo immunisation of HLA-A2.1 transgenic mice generated a specific CTL response against both hTERT peptides. The induction of CTL responses in vitro and the susceptibility to lysis of tumour cells of various origins hTERT CTL suggest that hTERT could serve as a universal cancer vaccine. Thus, a claimed universal vaccine for treating tumours of various origin comprises at least 1 hTERT peptide in an amount effective for initiating and enhancing a CTL response against cancer cells. The is 7-15 amino acid residues in length and may be modified to enhance binding to the major histocompatibility complex. Also claimed is a method for inducing and enhancing a CTL response against cancer cells, comprising harvesting blood leucocytes, pulsing with hTERT, and contacting cancer cells with the pulsed leucocytes. A method for targeting CTL to cancer cells is also claimed, and involves administering a hTERT peptide mammalian, especially a cancer patient.

Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 4; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0;

RAPRCRAVRSLSRSHYREVLPATFVRRLGPGQWRLVORGDPAAFRALVAQCLVCPVW 60
 RAPRCRAVRSLSRSHYREVLPATFVRRLGPGQWRLVORGDPAAFRALVAQCLVCPVW 60
 RPPPAAPSFQVSCLELVARVLRQLCERGAKNVLAFFGALLDGCARGPPEAFTTSVR 120
 RPPPAAPSFQVSCLELVARVLRQLCERGAKNVLAFFGALLDGCARGPPEAFTTSVR 120
 LPNTVTDALRGSGAWGLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPLVQLGA 180
 LPNTVTDALRGSGAWGLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPLVQLGA 180
 JARPPPHASGPRRLGGERAWNSVREAGVPLGLPAPGARRGGSASRSPLPKRRR 240
 JARPPPHASGPRRLGGERAWNSVREAGVPLGLPAPGARRGGSASRSPLPKRRR 240
 APERTPVQGSWAHPGTRGSDRGFCVVSAPARPAEATSLGALSGTRHSHPSVG 300
 APERTPVQGSWAHPGTRGSDRGFCVVSAPARPAEATSLGALSGTRHSHPSVG 300
 HAGPSTSEPPRPWDTPCPVVAETKHFYSSGDKQLRPSFLLSRPSLTGARRL 360
 HAGPSTSEPPRPWDTPCPVVAETKHFYSSGDKQLRPSFLLSRPSLTGARRL 360
 IFLSGRPMWPGTPRLPLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
 IFLSGRPMWPGTPRLPLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
 GVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSPPQVYGFVRACLRLRVPPLGWS 480
 GVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSPPQVYGFVRACLRLRVPPLGWS 480
 IRRFLRNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREI 540
 IRRFLRNTKFTSLGKHAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREI 540
 FLHLWMSVYVVELLRSFFVTETTFOKNLPFYRKSVMSKQSGIQRHKLKVQIRE 600
 FLHLWMSVYVVELLRSFFVTETTFOKNLPFYRKSVMSKQSGIQRHKLKVQIRE 600
 AEVQHRREARPALLTSRLRFIPKPDGLRPVIMNDYVVGARTFREKRAERLTSRKA 660
 AEVQHRREARPALLTSRLRFIPKPDGLRPVIMNDYVVGARTFREKRAERLTSRKA 660
 VLYNERARRPGLGASVGLDDIHRANRTFVLVRAQDPPPELYFKVDVTGAYDTI 720
 VLYNERARRPGLGASVGLDDIHRANRTFVLVRAQDPPPELYFKVDVTGAYDTI 720
 RLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPQYMRQFVAHL 780
 RLTEVIASIIKPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPQYMRQFVAHL 780
 SPLRDVAVIEOSSLSINEASSGLFDVFLRFMCHHVRIRGKSVQCGIPQGSILSTL 840
 SPLRDVAVIEOSSLSINEASSGLFDVFLRFMCHHVRIRGKSVQCGIPQGSILSTL 840
 LCYGDWENKLPAGTRRGGLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVEYGVVNL 900
 LCYGDWENKLPAGTRRGGLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVEYGVVNL 900
 VVNPFPVEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVDSDYSSYARTSIRASLT 960
 VVNPFPVEDEALGGTAFVQMPAHGLFPMCGLLDTRTLEVDSDYSSYARTSIRASLT 960
 FKAGNNRRKLPFVLRILKCHSLFDLQVNSLQTVCTNIYKILLIQAIRFACVQLP 1020
 FKAGNNRRKLPFVLRILKCHSLFDLQVNSLQTVCTNIYKILLIQAIRFACVQLP 1020
 QVKNPFTFFLRVSDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWICHQAFLL 1080
 QVKNPFTFFLRVSDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWICHQAFLL 1080
 RHRYVYVPLLSRLTAQTLQSRKLPGLTILTALEAANPALPSDFKTLILD 1132

Db 1081 KLTRHRYVYVPLLSRLTAQTLQSRKLPGLTILTALEAANPALPSDFKTLILD 1
 RESULT 11
 AAE29226
 ID AAE29226 standard; protein; 1132 AA.
 XX AAE29226;
 XX 27-JAN-2003 (first entry)
 DT Human telomerase reverse transcriptase (TERT).
 DE Carbohydrate antigen; alpha(1,3)galactosyltransferase; alpha1,3
 KW transgenic; alpha(1,2)fucosyltransferase; alpha1,2FT; human; en
 KW telomerase reverse transcriptase.
 XX Homo sapiens.
 OS WO200274948-A2.
 PN 26-SEP-2002.
 PD 21-MAR-2002; 2002WO-CA000378.
 PF 21-MAR-2001; 2001US-0277811P.
 PR (GERO-) GERON CORP.
 PA Denning C. Clark AJ, Schiff JM;
 XX WPI; 2002-759895/82.
 DR N-PSDB; RAD46821.
 DR Mammalian cells, useful for producing animal tissues with carbo
 PT antigens that are compatible for transplantation into human pat
 PT Disclosure; Page 34; 71pp; English.
 PS The invention relates to animal tissues with carbohydrate anti
 CC are compatible for transplantation into human patients. The mam
 CC cell is inactivated homozygously for expression of alpha(1,3)ga
 CC transferase (alpha1,3GT) gene and comprises a transgene for alp
 CC fucosyltransferase (alpha1,2FT). It is useful for producing an
 CC with carbohydrate antigens that are compatible for producing an
 CC human patients. The present sequence is human telomerase reverse
 CC transcriptase (TERT) used in the invention
 XX Sequence 1132 AA;
 SQ
 Query Match 100.0%; Score 5961; DB 5; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0;
 QY 1 MPAPRCRAVRSLSRSHYREVLPATFVRRLGPGQWRLVORGDPAAFRALVAQCI
 Db 1 MPAPRCRAVRSLSRSHYREVLPATFVRRLGPGQWRLVORGDPAAFRALVAQCI
 QY 61 DARPPPAAPSFQVSCLELVARVLRQLCERGAKNVLAFFGALLDGCARGPPEAF
 Db 61 DARPPPAAPSFQVSCLELVARVLRQLCERGAKNVLAFFGALLDGCARGPPEAF
 QY 121 SYLNTVTDALRGSGAWGLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPL
 Db 121 SYLNTVTDALRGSGAWGLLRRVGDVLLVHLLARCALFVLVAPSCAYQVCGPPL
 QY 181 ATQAREPPPHASGPRRLGGERAWNSVREAGVPLGLPAPGARRGGSASRSPLP
 Db 181 ATQAREPPPHASGPRRLGGERAWNSVREAGVPLGLPAPGARRGGSASRSPLP
 QY 241 GAAPPERTPVQGSWAHPGTRGSDRGFCVVSAPARPAEATSLGALSGTRHS

APEPERTVGGSWAHGPRGRGSDRGFCVVSPPARPAEATSLEGALSGTRHSHPSVG 300
 HHAGPSTSRPRPDWPCPPVYATKHFLYSSGDKQLRPSFLLSLRPSLTGAREL 360
 HHAGPSTSRPRPDWPCPPVYATKHFLYSSGDKQLRPSFLLSLRPSLTGAREL 360
 TIFLGSPPMPTGTPRRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVILKTHCPLEAAVT 420
 TIFLGSPPMPTGTPRRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVILKTHCPLEAAVT 420
 TIFLGSPPMPTGTPRRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVILKTHCPLEAAVT 420
 AGVCAREKPGQSVAAPEEEDTPRRLLVQLLRQHSPPQVYGFVRACLRLRLVPPGLWS 480
 AGVCAREKPGQSVAAPEEEDTPRRLLVQLLRQHSPPQVYGFVRACLRLRLVPPGLWS 480
 NERBFLNNTKFIISLGHAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAEHLRREI 540
 NERBFLNNTKFIISLGHAKLSLOELTWKMSVRDCAWLRRSPGVGCVPAEHLRREI 540
 KFLHLMMSVYVVELLRFFVYTTTFOKNRLFFVRKSVWSKLSIGIRQHLKRVQURE 600
 KFLHLMMSVYVVELLRFFVYTTTFOKNRLFFVRKSVWSKLSIGIRQHLKRVQURE 600
 KFLHLMMSVYVVELLRFFVYTTTFOKNRLFFVRKSVWSKLSIGIRQHLKRVQURE 600
 EAEVQHREARPAALLTSRLRPIPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
 EAEVQHREARPAALLTSRLRPIPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVKA 660
 SVLNREARPPGLIGASVLGDDIHRAWRTFVLRVAQDPPPELYFKVDVTGAYDTI 720
 SVLNREARPPGLIGASVLGDDIHRAWRTFVLRVAQDPPPELYFKVDVTGAYDTI 720
 DRLEVIASIIKQNTYCVRYAVVQAAHGHVRKAFKSHVSTLTDLPQMRQFVAHL 780
 DRLEVIASIIKQNTYCVRYAVVQAAHGHVRKAFKSHVSTLTDLPQMRQFVAHL 780
 TSPLDAVVIQSSSNEASSGLFDVPLRFMCHHVRIRGKSVYQCGIPQSSILSTL 840
 TSPLDAVVIQSSSNEASSGLFDVPLRFMCHHVRIRGKSVYQCGIPQSSILSTL 840
 ILCYGMENKLFAGIRDDGLLRLVDDFLVTPHLTHAKTFLRLVGVPEYGCVVNL 900
 ILCYGMENKLFAGIRDDGLLRLVDDFLVTPHLTHAKTFLRLVGVPEYGCVVNL 900
 TVNFFVEDEALGTTAFVQMPAHGLFPWCGLLDTRTLEVSQDYSYASRTSRASITP 960
 TVNFFVEDEALGTTAFVQMPAHGLFPWCGLLDTRTLEVSQDYSYASRTSRASITP 960
 IFKAGNMRKLFGLVRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVQLP 1020
 IFKAGNMRKLFGLVRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVQLP 1020
 IQVWKNPTFLRVIDSTSLCYSLKAKNAGSLGAKGAGPLPSEAVOMLCHQAFLL 1080
 IQVWKNPTFLRVIDSTSLCYSLKAKNAGSLGAKGAGPLPSEAVOMLCHQAFLL 1080
 RHRVTVPLLSRLTAQTLQSLKPLGTTTLTALEAANPALPDSFDTILD 1132
 RHRVTVPLLSRLTAQTLQSLKPLGTTTLTALEAANPALPDSFDTILD 1132

ndard; protein; 1132 AA.

(first entry)

rase reverse transcriptase (TERT).

everse transcriptase; TERT; cytostatic; apoptosis;
 inhibitor; antisense oligonucleotide; antisense technology.

XX WO200188198-A1.
 XX 22-NOV-2001.
 XX 15-MAY-2001; 2001WO-US015774.
 XX 16-MAY-2000; 2000US-00572423.
 XX 07-DEC-2000; 2000US-00733294.
 XX (ISIS-) ISIS PHARM INC.
 XX Monia BP, Gaarde WA, Freier SM, Wancewicz E;
 XX WPI; 2002-075321/10.
 XX N-PSDB; AAS96607.
 XX New compound targeted to nucleic acid molecule encoding telomere
 XX transcriptase (TERT), which specifically hybridizes with and in
 XX expression of TERT, useful for modulating apoptosis and inhibit
 XX growth.
 XX Disclosure; Page 100-105; 154pp; English.
 XX The invention describes a compound, 8-50 nucleobases in length
 XX to a nucleic acid molecule encoding human TERT (telomerase reve
 XX transcriptase), where the compound specifically hybridizes with
 XX inhibits the expression of TERT. A series of oligonucleotides w
 XX designed to target different regions of the human TERT RNA. The
 XX nucleotides in length and composed of a central gap region cons
 XX ten 2'-deoxynucleotides, flanked on both sides (5' and 3' direc
 XX five-nucleotide wings. The wings were composed of 2'-methoxyeth
 XX MOE) nucleotides. The compounds were analysed for their effect
 XX TERT mRNA levels by reverse transcriptase (RT)-polymerase chain
 XX (PCR). The compound is useful for inhibiting the expression of
 XX cells or tissues, for treating a human having disease or condit
 XX associated with TERT, for modulating apoptosis, for inhibiting
 XX growth (preferably, cancer cell growth), in antisense therapy a
 XX diagnostics and therapeutics. This is the amino acid sequence o
 XX telomerase reverse transcriptase (TERT), described in the metho
 XX invention

SQ Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 5; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLGPGQWRLVQGDPAAFRALVAQCI
 Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRLGPGQWRLVQGDPAAFRALVAQCI
 Qy 61 DARPPPAAPSPFVSCUKELVARVLOLRCERGAKNVLAFGALLDARGGPPPAI
 Db 61 DARPPPAAPSPFVSCUKELVARVLOLRCERGAKNVLAFGALLDARGGPPPAI
 Qy 121 SYLPTNTVTDALRGSGAWGLLRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPI
 Db 121 SYLPTNTVTDALRGSGAWGLLRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPI
 Qy 181 ATOARPPPHASGPRRLGGERAWNHVSREAGVPLGLPAPGARRRGGASRLPLF
 Db 181 ATOARPPPHASGPRRLGGERAWNHVSREAGVPLGLPAPGARRRGGASRLPLF
 Qy 241 GAAPERTPVGGSWAHGPRGRGSDRGFCVVSPPARPAEATSLEGALSGTRHS
 Db 241 GAAPERTPVGGSWAHGPRGRGSDRGFCVVSPPARPAEATSLEGALSGTRHS
 Qy 301 RQHAGPSTSRPRPDWPCPPVYATKHFLYSSGDKQLRPSFLLSLRPSLT
 Db 301 RQHAGPSTSRPRPDWPCPPVYATKHFLYSSGDKQLRPSFLLSLRPSLT
 Qy 361 VETIFLGSPPMPTGTPRRRLPRLPQRYWQMRPLFLELLGNHQAQCPYGVILKTHCP

-A2-

481 RHNERFLRNTKFI SLGKHA KLSLQELTWKMSVRDCAWLRRSPGVGCVPAAEHR: QY

|||||
 NERFLNTKAFISLGHAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEHRLREBI 540
 KFLHMLSVYVVELLRFFYYTETTFQKNRFFFYKRSVMSKIQSIGIRQHLKRVOLRE 600
 KFLHMLSVYVVELLRFFYYTETTFQKNRFFFYKRSVMSKIQSIGIRQHLKRVOLRE 600
 EAEVROHREARPAALLTSRLRIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
 EAEVROHREARPAALLTSRLRIPKPDGLRPIVNMDDYVVGARTFRREKRAERLTSRVKA 660
 SVLNYERARRPGLIGASVLGDDTHRAWRTEFLVRVRAQDPEPELYFVKVDMVTGAYDTI 720
 SVLNYERARRPGLIGASVLGDDTHRAWRTEFLVRVRAQDPEPELYFVKVDMVTGAYDTI 720
 DRLTEVTSIIKPNQTYCVRYAVVQKAAHGHVRKAFKSHVSTLTDLQPMYRQFVAHL 780
 DRLTEVTSIIKPNQTYCVRYAVVQKAAHGHVRKAFKSHVSTLTDLQPMYRQFVAHL 780
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 TSPURDAVVIQSSSINEASSGLFDVFLRPMCHHVAIRKSVYVQCGIQSGISLSTL 840
 SLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRTLVRGVPEYGCNVNL 900
 SLCYGMENKLFAGIRRDGLLLRLVDDFLVTPHLTHAKTFLRTLVRGVPEYGCNVNL 900
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 TVNFPVEDALGTAFTVQMPAHGLFPWCGLLDTLRLVQSDYSYARTSIRASLTF 960
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 3FKAGRNMRKLFQVLEKCHSLFDLDQVNSLQTVCTNIYKILLQAYRHACVLOLP 1020
 QQWKNPTFFLRVISTASLCYSILKAKNAGMSLGAAGPLPSEAVQWLCHQAFLL 1080
 QQWKNPTFFLRVISTASLCYSILKAKNAGMSLGAAGPLPSEAVQWLCHQAFLL 1080
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 TRHRVYVPLLSRTAQTLQSRKLPOTTLTALAAANPALPSDFKTLTD 1132

standard; protein; 1132 AA.

(first entry)

reverse transcriptase.

reverse transcriptase; TERT: enzyme; RNA interference;
 interfering RNA; siRNA; cancer; tumour; cytostatic; contraceptive;
 aseptic; antifertility; fungicide; antiparasitic;
 itory; human; gene therapy.

1.

1-A2.

2002WO-US033146.

2001US-0345326P.

2002US-0359196P.

2002US-0383195P.

1 ROCHESTER.

PI Rowley PT;
 XX WPI: 2003-403289/38.
 DR N-PSDB; ACC57552.
 XX
 PT Novel nucleic acid encoding or comprising interfering RNAs which
 PT telomerase RNA, useful for inhibiting telomerase activity for t
 PT cancer, infertility and disorders of the immune system.
 XX
 PS Disclosure; Fig 4; 52pp; English.
 XX
 CC The present sequence is that of human telomerase reverse trans-
 CC (TERT). The invention relates to the discovery that double-str-
 CC interfering RNAs, such as short interfering RNAs (siRNA), which
 CC telomerase RNA or TERT mRNA are capable of inhibiting telomeras-
 CC activity. Inhibition of telomerase in cancer cells leads to tel-
 CC shortening, end-to-end chromosomal fusion, and apoptosis. Inter-
 CC telomerase activity can also be used for treatment of infertility
 CC conception or sterility, for immunosuppression, for treat-
 CC yeast, parasite and fungal infections, and in anti-inflammat-
 CC As telomerase is active in a limited number of cell types, e.g.
 CC cells, germ-line cells, certain stem cells of the haematopoietic
 CC and B cells, sun-damaged skin, and proliferative cervix, most n
 CC cells are not affected by telomerase RNA interference therapy
 XX
 SQ Sequence 1132 AA;
 Query Match 100.0%; Score 5961; DB 6; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0;
 QY 1 MPRAPCRCAVSLRLSHRYEVLPLATFVRLGPOGWRVQGRDPAAPRALVAQC
 Db 1 MPRAPCRCAVSLRLSHRYEVLPLATFVRLGPOGWRVQGRDPAAPRALVAQC
 QY 61 DARPPPAAPSFRQVSCIKELVARVLQRLCERGAKNVLAFFGALLDGGAPGPEA
 Db 61 DARPPPAAPSFRQVSCIKELVARVLQRLCERGAKNVLAFFGALLDGGAPGPEA
 QY 121 SYLNTVTVDALRGSGAGMLLRRVGDVVLVHLLARCALFVLVAPSCAVQVCGPP
 Db 121 SYLNTVTVDALRGSGAGMLLRRVGDVVLVHLLARCALFVLVAPSCAVQVCGPP
 QY 181 ATQARPPPHASGPRRLGCEAMNHSVREAGVPLGLPAPGARRRGGASRLPL
 Db 181 ATQARPPPHASGPRRLGCEAMNHSVREAGVPLGLPAPGARRRGGASRLPL
 QY 241 GAAPERTPVQGSWAHPGRTGPRSDRGFCVSPARPAEATSLEGALSOTRH
 Db 241 GAAPERTPVQGSWAHPGRTGPRSDRGFCVSPARPAEATSLEGALSOTRH
 QY 301 ROHHAGPPSTPRPMDTCPVYATKHPYSSGDKQELRPSFLSSLRPSL
 Db 301 ROHHAGPPSTPRPMDTCPVYATKHPYSSGDKQELRPSFLSSLRPSL
 QY 361 VETIFLGSRRPMPGTPRLPRLPQRYWQMRPLFLELGNHAQCPYGVLLKTHCP
 Db 361 VETIFLGSRRPMPGTPRLPRLPQRYWQMRPLFLELGNHAQCPYGVLLKTHCP
 QY 421 PAAGVCAREKPGQSVAAPEEEDTDPRLLVOLLROHSSFPWQYGFVRACLRLVPI
 Db 421 PAAGVCAREKPGQSVAAPEEEDTDPRLLVOLLROHSSFPWQYGFVRACLRLVPI
 QY 481 RHNERFLRNTKFIISLGHAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEH
 Db 481 RHNERFLRNTKFIISLGHAKLSLOELTWKMSVRDCAWLRSPGVCVPAAEH
 QY 541 LAKFLHMLSVYVVELLRFFYYTETTFQKNRFFFYKRSVMSKIQSIGIRQHLK
 Db 541 LAKFLHMLSVYVVELLRFFYYTETTFQKNRFFFYKRSVMSKIQSIGIRQHLK
 QY 601 LSEAEVROHREARPAALLTSRLRIPKPDGLRPIVNMDDYVVGARTFRREKRAERL

AEVQHQREARPAALLTSRLRFTPKDGLRPIVNMVYVVGARTFRREKRAERLTSRVA 660
 VLNTERARRPGLLGASVGLDDIIHRAMRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
 VLNTERARRPGLLGASVGLDDIIHRAMRTFVLVRAQDPPPELYFVKVDVTGAYDTI 720
 RLTEVIASIIKPPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPQYMRQFVAHL 780
 RLTEVIASIIKPPQNTYCVRRYAVVQKAAHGHVRKAFKSHVSTLTDLPQYMRQFVAHL 780
 SPLRDVAVIEOSSINEASSGLFDVFLRFMCHHAVIRGKSYVOCQGIPOGSIILSTL 840
 SPLRDVAVIEOSSINEASSGLFDVFLRFMCHHAVIRGKSYVOCQGIPOGSIILSTL 840
 LCYGDMENKLPAGIRRDGLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVPYGCYVNL 900
 LCYGDMENKLPAGIRRDGLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVPYGCYVNL 900
 VVNPVDEALGGTAFVQMPAHGLFPWCGLLDFTLEVOQSDYSSYARTSIRASLTF 960
 VVNPVDEALGGTAFVQMPAHGLFPWCGLLDFTLEVOQSDYSSYARTSIRASLTF 960
 FKAGNNRRKLPGLVRLKCHSLFDLDQVNSLQTVCTNIIYKILLQAVREHACVLQLP 1020
 FKAGNNRRKLPGLVRLKCHSLFDLDQVNSLQTVCTNIIYKILLQAVREHACVLQLP 1020
 QVKNPTFFLRVISTDASLCYSILKAKNAGMSLGAKGAAGLPSEAVQWMLCHQAFLL 1080
 QVKNPTFFLRVISTDASLCYSILKAKNAGMSLGAKGAAGLPSEAVQWMLCHQAFLL 1080
 RHRVTVYVLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132
 RHRVTVYVLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILD 1132

adard; protein; 1132 AA.

(first entry)

ase reverse transcriptase protein SEQ ID NO:2.

ase reverse transcriptase; enzyme; hTERT; chromosome 5;
 atulcer; epithelial cell migration promoter; wound;
 on; skin wound; lesion; burn; surgical incision; ulcer;
 all; keratinocyte; epidermal; mucosal.

12.

2002WO-US014867.

2001US-0289903P.

1 CORP.

lu C, Harley CB;

591/11.

2474.

for treating wounds and enhancing epithelization of a skin
 rises vector encoding telomerase reverse transcriptase or
 epithelial cells on a microparticle or a matrix.

page 32; 68pp; English.

CC The present invention describes a pharmaceutical composition (I) comprising a vector encoding telomerase reverse transcriptase (C an excipient or device, or comprises telomerase epithelial cell microparticle or a matrix suitable for topical administration or administration to a wound site. (I) has vulnary and anticulcer activities and can be used to promote epithelial cell migration useful for treating a wound and enhancing epithelization of a wound surface. The wound is especially skin wound including acute lesion as traumatic lesion, burn, or surgical incision, chronic lesion chronic venous ulcer, diabetic ulcer or compression ulcer and the is further monitored for closure. The telomerase activity or TEF expression is increased in epithelial cells at the site of treatment also in fibroblasts or endothelial cells at the site of treatment epithelial cells are especially keratinocytes. A polynucleotide TERT is useful for the preparation of a medicament for treatment wound or an epithelial surface in a human or animal. An epithelial with increased telomerase activity or increased expression of TEF useful for preparation of a medicament for the treatment of a wound human or animal. (I) is also useful for treating wounds of other epidermal surfaces including mucosal surfaces such as bronchus, nose, oesophagus, stomach, or intestine. The present sequence is human TERT (hTERT), which is given in the exemplification of the invention. hTERT is located to chromosome 5

Sequence 1132 AA;

Query Match 100.0%; Score 5961; DB 6; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0;

QY 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRLVQRGDPAAFRALVAQCI
 Db 1 MPRAPRCRAVRSLLRSHYREVLPATFVRRLGPGQWRLVQRGDPAAFRALVAQCI
 QY 61 DARPPAAPSPQVSCLEKELVARVLRQRCERGANVLAFCGALLDGAAGGPPPEAF
 Db 61 DARPPAAPSPQVSCLEKELVARVLRQRCERGANVLAFCGALLDGAAGGPPPEAF
 QY 121 SYLPTNTVDALRGSGAWGLLRLRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPL
 Db 121 SYLPTNTVDALRGSGAWGLLRLRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPL
 QY 181 ATQARPPPHASGPRRLRGCEANHSVREAGVPLGLPAPGARRRGGASRSLSPLP
 Db 181 ATQARPPPHASGPRRLRGCEANHSVREAGVPLGLPAPGARRRGGASRSLSPLP
 QY 241 GAAPPERTPVQGGWAHFGTRGSDRGFCVVSAPARPAEATSLGALSCTRHS
 Db 241 GAAPPERTPVQGGWAHFGTRGSDRGFCVVSAPARPAEATSLGALSCTRHS
 QY 301 ROHAGPSTSRPPRPWDTPCPVVAETKHFLYSSGDKQLRPSFLLSLRPSLT
 Db 301 ROHAGPSTSRPPRPWDTPCPVVAETKHFLYSSGDKQLRPSFLLSLRPSLT
 QY 361 VETIFLGRPMWPGTFRRLPLRPQRYWQMRPLFLELLGNHACQPYGVLLKTHCPL
 Db 361 VETIFLGRPMWPGTFRRLPLRPQRYWQMRPLFLELLGNHACQPYGVLLKTHCPL
 QY 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSPPWQVYGFVRACLRRLVPP
 Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSPPWQVYGFVRACLRRLVPP
 QY 481 RHNERFLRNTKFTISLGHAKLSLQELTWKMSVRDCAWLRRSPGVCVPAAEHRI
 Db 481 RHNERFLRNTKFTISLGHAKLSLQELTWKMSVRDCAWLRRSPGVCVPAAEHRI
 QY 541 LAKFLHMLSVVVELLSFFVTTTTFQKNRLLFFYRKSVMKLSQSIGIRQLKRY
 Db 541 LAKFLHMLSVVVELLSFFVTTTTFQKNRLLFFYRKSVMKLSQSIGIRQLKRY
 QY 601 LSEAEVROHREARPAALLTSRLRFTPKDGLRPIVNMVYVVGARTFRREKRAERLT
 Db 601 LSEAEVROHREARPAALLTSRLRFTPKDGLRPIVNMVYVVGARTFRREKRAERLT

VLNYERARRPGLLGASVIGLDDIHRAWRTFVLVRVAQDPPPELYEFVKVDVTGAYDTI 720
VLNYERARRPGLLGASVIGLDDIHRAWRTFVLVRVAQDPPPELYEFVKVDVTGAYDTI 720
RLTEVIASIIKQNTYCVRRYAVQKAAHGVKAFKSHVSTLTDLQPYMRQFVAHL 780
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SPLRDAVVIEQSSSINEASSGLFDVFLRFMCHHAVRIRGKSVQCQGIPOGSIILSTL 840
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LCYGMENKLFAGIRRDGILLRLVDDFLLVTPHLTHAKTFLRTLVRGVPYGCVVNL 900
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VVNPFVEDEALGGTAFVQMPAHGLFPWCGLLDDTLEVSQDYSYARTSIRASLTF 960
VVNPFVEDEALGGTAFVQMPAHGLFPWCGLLDDTLEVSQDYSYARTSIRASLTF 960
FKAGNMRRKLFVGLRLKCHSIFLDLQVNSLQTVCTNIYKILLQAYRPHACVQLP 1020
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QVWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
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RHRVTYVPLGSLRTRTAQQLSRKLP GTTLTALERAAANPALPSDFKTILD 1132
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GenCore version 5.1.6
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in search, using sw model

April 22, 2004, 00:12:11 ; Search time 26 Seconds
(without alignments)
2247.715 Million cell updates/sec

JS-09-424-686f-2

3961

MPRAPRCRAVRLSHVRE.....TALRAANPALPSDKTILD 1132

3LOSUM62

lapop 10.0 , Gapext 0.5

89414 segs, 51625971 residues

uts satisfying chosen parameters: 389414

mgth: 0

mgth: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Issued Patents AA.*

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: /cgn2_6/ptodata/2/iaa/5B COMB.pcp.*
: /cgn2_6/ptodata/2/iaa/6A COMB.pcp.*
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: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pcp.*
: /cgn2_6/ptodata/2/iaa/backfiles1.pcp.*

s the number of results predicted by chance to have a
ver than or equal to the score of the result being printed,
ved by analysis of the total score distribution.

SUMMARIES

* query atrch	Length	DB	ID	Description
00.0	1132	3	US-08-851-843A-225	Sequence 225, App
00.0	1132	3	US-08-974-549A-2	Sequence 2, Appli
00.0	1132	3	US-08-854-050-225	Sequence 225, App
00.0	1132	4	US-09-430-323-225	Sequence 225, App
00.0	1132	4	US-09-128-354-2	Sequence 2, Appli
00.0	1132	4	US-09-675-321-2	Sequence 2, Appli
00.0	1132	4	US-09-052-919-2	Sequence 2, Appli
00.0	1132	4	US-08-912-951-2	Sequence 2, Appli
00.0	1132	4	US-09-402-181B-2	Sequence 2, Appli
00.0	1132	4	US-09-721-456-2	Sequence 2, Appli
00.0	1132	4	US-09-953-052-2	Sequence 2, Appli
00.0	1154	3	US-08-974-549A-611	Sequence 611, App
00.0	1154	4	US-08-912-951-323	Sequence 323, App
00.0	1154	4	US-09-402-181B-611	Sequence 611, App
00.0	1154	4	US-09-721-456-611	Sequence 611, App
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00.0	1285	4	US-08-912-951-314	Sequence 314, App
00.0	1285	4	US-09-402-181B-600	Sequence 600, App
00.0	1285	4	US-09-721-456-600	Sequence 600, App

28	5952	99.8	1132	3	US-08-974-549A-344	Sequence
29	5952	99.8	1132	4	US-09-402-181B-344	Sequence
30	5952	99.8	1132	4	US-09-721-456-344	Sequence
31	5952	99.8	1407	3	US-08-974-549A-628	Sequence
32	5952	99.8	1407	4	US-08-912-951-334	Sequence
33	5952	99.8	1407	4	US-09-402-181B-628	Sequence
34	5952	99.8	1407	4	US-09-721-456-628	Sequence
35	4052	68.0	807	3	US-08-974-549A-5	Sequence
36	4052	68.0	807	4	US-08-912-951-5	Sequence
37	4052	68.0	807	4	US-09-402-181B-5	Sequence
38	4052	68.0	807	4	US-09-721-456-5	Sequence
39	3819.5	64.1	1003	3	US-08-851-843A-217	Sequence
40	3819.5	64.1	1003	3	US-08-974-549A-336	Sequence
41	3819.5	64.1	1003	3	US-08-854-050-217	Sequence
42	3819.5	64.1	1003	4	US-09-430-323-217	Sequence
43	3819.5	64.1	1003	4	US-09-402-181B-336	Sequence
44	3819.5	64.1	1003	4	US-09-721-456-336	Sequence
45	3134	52.6	622	4	US-09-582-924B-12	Sequence

ALIGNMENTS

RESULT 1

US-08-851-843A-225
; Sequence 225, Application US/08851843A
; Patent No. 6093809

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morlin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 225:

CHARACTERISTICS:
1132 amino acids
ino acid
linear
PE: protein
25

100.0%; Score 5961; DB 3; Length 1132;
ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RPPPAAPFRQVSKLKLVARLQRLCERCAKNVLAFFALLDGCARGPPPEAFTTSVR 120
LPNTVTDALRGSGAWGLLLRRVGDVLLHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
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HAGPSTSPRPWDTPCPVVAETKHFIYSSGDEQLRPSFLLSLPSLTGARRL 360
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TIFLGRPMWPGTRPLRPLQRYWQMRPLFELGLGNHQAQCPYGVLLKTHCPLRAVT 420
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JERRFLNTKFTSLGKHAKLSQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREI 540
JERRFLNTKFTSLGKHAKLSQELTWKMSVRDCAWLRRSPGVGCVPAAEHRLREI 540
FLHLMMSVYVVELLSRFFVTTTFOKNRPFYRKSVMKLSQSIGIROHLKRVQLRE 600
FLHLMMSVYVVELLSRFFVTTTFOKNRPFYRKSVMKLSQSIGIROHLKRVQLRE 600
JAEVROHREARPALLTSRLRFTPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVA 660
JAEVROHREARPALLTSRLRFTPKPDGLRPIVNMVYVVGARTFRREKRAERLTSRVA 660
JVNLYERARRPGLGASVGLDDIHRANWTFVLVRAQDPPPELYPKVDVDTGAYDTI 720
JVNLYERARRPGLGASVGLDDIHRANWTFVLVRAQDPPPELYPKVDVDTGAYDTI 720
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JRLTEVIAIIPQNTYCVRRYAVVQAAHGVKAFKSHVSTLTDLPYMWQFVAHL 780
JSPLRDAVIEQSSSNEASSGLFDVFLRPMCHHAVIRKGSYVQCGIPQGSILSTL 840
JSPLRDAVIEQSSSNEASSGLFDVFLRPMCHHAVIRKGSYVQCGIPQGSILSTL 840
JLCYGDWMENKLFAGIRRDGLLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPEYGCVVNL 900
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JVNFPVEDEALGCTAFVQMPAHGLFPWCGLLDDTRTLEVQSDYSYARTSRLTTF 960
JVNFPVEDEALGCTAFVQMPAHGLFPWCGLLDDTRTLEVQSDYSYARTSRLTTF 960

Db 901 RKTUVNFFVEDEALGCTAFVQMPAHGLFPWCGLLDDTRTLEVQSDYSYARTSI
QY 961 NGEFKAGNMRKLFGLRLKCHSLFLDLQVNSLQVCTNIYKILLQYRPHA
Db 961 NGEFKAGNMRKLFGLRLKCHSLFLDLQVNSLQVCTNIYKILLQYRPHA
QY 1021 FHQQWKVNPTFFLRVISDTASLCYSILKAKNAGMSLGAAGPPLPSEAVOWLC
Db 1021 FHQQWKVNPTFFLRVISDTASLCYSILKAKNAGMSLGAAGPPLPSEAVOWLC
QY 1081 KLTRHRTVYVPLLGSRLTAQTQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1
Db 1081 KLTRHRTVYVPLLGSRLTAQTQLSRKLPGLTTLTALEAAANPALPSDFKTILD 1

RESULT 2

US-08-974-549A-2
; Sequence 2, Application US/08974549A
; Patent No. 6166178
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; PRIOR APPLICATION DATA:

IN NUMBER: WO PCT/US97/17885
 E: 01-OCT-1997
 NT INFORMATION:
 le, Randolph Ted
 ON NUMBER: 36,429
 DOCKET NUMBER: 015389-002610US
 ATION INFORMATION:
 (415) 576-0200
 (415) 576-0300
 R SEQ ID NO: 2:
 RACTERISTICS:
 132 amino acids
 no acid
 linear
 E: protein

100.0%; Score 5961; DB 3; Length 1132;
 larity 100.0%; Pred. No. 0;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 781 QETSPRLDVAVIEOSSLINEASSGLFDVFLRFMCHHVRIRGKSYVQCOGIPQG:
 QY 841 LCSLCYGDMMENKUPAGIRRDGLLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVEY:
 DB 841 LCSLCYGDMMENKUPAGIRRDGLLLRLVDDFLLVTPHLLTHAKTFLRTLVRGVEY:
 QY 901 RKTWNFPVDEALGGTAFVQMPAHGLFPMCGLLLDTRTLEVDQSSYARTSI:
 DB 901 RKTWNFPVDEALGGTAFVQMPAHGLFPMCGLLLDTRTLEVDQSSYARTSI:
 QY 961 NRGFKAGNNRRKLFGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHA:
 DB 961 NRGFKAGNNRRKLFGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHA:
 QY 1021 FHOQVWKNPTFFFLRVISDTSASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCE:
 DB 1021 FHOQVWKNPTFFFLRVISDTSASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCE:
 QY 1081 KLTRHRVTVYVPLLGSLRTAQTLSRLPGTTLTALEAAANPALPSPDKTILD 11
 DB 1081 KLTRHRVTVYVPLLGSLRTAQTLSRLPGTTLTALEAAANPALPSPDKTILD 11

RESULT 3

US-08-854-050-225
 ; Sequence 225, Application US/08854050
 ; Patent No. 6261836
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; APPLICANT: Lingner, Joachim
 ; APPLICANT: Nakamura, Toru
 ; APPLICANT: Chapman, Karen B.
 ; APPLICANT: Morin, Gregg B.
 ; APPLICANT: Harley, Calvin
 ; APPLICANT: Andrews, William H.
 ; NUMBER OF SEQUENCES: 225
 ; TITLE OF INVENTION: No. 6261836el Telomerase
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States of America
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/854,050
 ; FILING DATE: 09-MAY-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/851,843
 ; FILING DATE: 06-MAY-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/846,017
 ; FILING DATE: 25-APR-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/844,419
 ; FILING DATE: 18-APR-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/724,643
 ; FILING DATE: 01-OCT-1996
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Apple, Randolph T.

ION NUMBER: 36,429
DOCKET NUMBER: 015389-002930US

ATION INFORMATION:

(415) 576-0200

(415) 576-0300

IR SEQ ID NO: 225:

ACTERISTICS:

.132 amino acids

no acid

linear

PE: protein

;

ilarity 100.0%; Score 5961; DB 3; Length 1132;

Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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!>OLOGY: linear
!>TYPE: protein
!>DESCRIPTION: SEQ ID NO: 225:

100.0%; Score 5961; DB 4; Length 1132;
larity 100.0%; Pred. No. 0;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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VWVFFVEDEALGGTAFVQMPAHGLFPMCGLLLDTRTLEVDYSSYARTSIRASLTF 960

QY 961 NRGFAGNRMRKLFGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRPHA
Db 961 NRGFAGNRMRKLFGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRPHA
QY 1021 FHOQVKNPTFFFLRVISDTSASLCYSILKAKNAGMSLGAAGPLPSEAVOMLCI
Db 1021 FHOQVKNPTFFFLRVISDTSASLCYSILKAKNAGMSLGAAGPLPSEAVOMLCI
QY 1081 KLTRHRVTVYVPLLGSLRTAQTOLSRKLPCTTTLTALEAAANPALPSDFKTILD 1:
Db 1081 KLTRHRVTVYVPLLGSLRTAQTOLSRKLPCTTTLTALEAAANPALPSDFKTILD 1:

RESULT 5

US-09-128-354-2
; Sequence 2, Application US/09128354
; Patent No. 6337200
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Genon Corporation
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE REFERENCE: 015389-003310US
; CURRENT APPLICATION NUMBER: US/09/128,354
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 08/851,843
; EARLIER FILING DATE: 1997-05-06
; EARLIER APPLICATION NUMBER: US 08/854,050
; EARLIER FILING DATE: 1997-05-09
; EARLIER APPLICATION NUMBER: US 08/911,312
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: US 08/912,951
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: US 08/915,503
; EARLIER FILING DATE: 1997-08-14
; EARLIER APPLICATION NUMBER: WO PCT/US97/17618
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: WO PCT/US97/17885
; EARLIER FILING DATE: 1997-10-01
; EARLIER APPLICATION NUMBER: US 08/974,549
; EARLIER FILING DATE: 1997-11-19
; EARLIER APPLICATION NUMBER: US 08/974,584
; EARLIER FILING DATE: 1997-11-19
; EARLIER APPLICATION NUMBER: US 09/052,864
; EARLIER FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-354-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;

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Db 1 MPRAPRCRAVRSILRSHRYEVLPLATFVRRLGQGWRLVQRGDPAAPRALVAQCL
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Db 61 DARPPAAPSRQVSCIKELVARVLQRLCERGAKNVLAFGFALLDARGSPPEAF
QY 121 SYLPNTVTDALRGSGAGLLLRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPL
Db 121 SYLPNTVTDALRGSGAGLLLRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPL
QY 181 ATCARPPPHASGPRRLRCERAMNHSVREAGVPLGLPAPGARRRGGSASRLPLP
Db 181 ATCARPPPHASGPRRLRCERAMNHSVREAGVPLGLPAPGARRRGGSASRLPLP
QY 241 GAAPPERTVQGSWAHPGRTGPDGFCVSPARPABEATSLEGALSGTRHS:

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 :HAGPSTSRPPPDWTPCPCPPVYAETHFLYSSGDKBQELRSPFLLSSRLRPSLTGARRL 360
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Publication US/09675321

735

TION.

1000

la, Federal C.A.

Iron Corporation

RESULTS: Methods ar

CTION: Response

015389-003500E

ATION NUMBER: 175

DATE. 2000-09-

DATE: 2000-03-01
 TIME: 11:00 AM

MEMBER: US 6

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; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-675-321-2

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Query Match      100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;
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Db	601	LSEAEVRQHREARPALLSRLRFPKPDGLRPIVNMQYVVGARFTRFKEKAERL
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Qy	721	PODRLETVIASIIRPQNTYCVRRYAVVQKAHGHVRKAFKSHVSTLTDLOPYMR
Db	721	PODRLETVIASIIRPQNTYCVRRYAVVQKAHGHVRKAFKSHVSTLTDLOPYMR
Qy	781	QZTSFLRDAVVIQSSSLNEASSGJFDVFLRFMCHHAVIRGKSYVQCQIGPOG
Db	781	QZTSFLRDAVVIQSSSLNEASSGJFDVFLRFMCHHAVIRGKSYVQCQIGPOG
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lication US/09052919
1650
ATION:
Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
VENTION: Antisense Compositions for Detecting and
ENTON: Inhibiting Telomerase Reverse Transcriptase
QUENCES: 72
ICE ADDRESS:
Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
San Francisco
California
USA
1-3834
ADABLE FORM:
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
ICATION DATA:
NN NUMBER: US/09/052,919
E: 31-MAR-1998
ATION: 435
ATION DATA:
NN NUMBER: US 08/724,643
E: 01-OCT-1996
ATION DATA:
NN NUMBER: US 08/844,419
E: 18-APR-1997
ATION DATA:
NN NUMBER: US 08/846,017
E: 25-APR-1997
ATION DATA:
NN NUMBER: US 08/851,843
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NN NUMBER: US 08/911,312
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E: 14-AUG-1997
ATION DATA:
NN NUMBER: US 08/915,503

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THRVTVPLLSGLRTAQOLSKRLPGTTLTALEAAANPALPSDFKTIILD 1132
THRVTVPLLSGLRTAQOLSKRLPGTTLTALEAAANPALPSDFKTIILD 1132

Application US/08912951
789
ATION:
Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
ENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
SEQUENCES: 335
CE ADDRESS:
Townsend and Townsend and Crew LLP
wo Embarcadero Center, 8th Floor
San Francisco
California
United States of America
1
ADABLE FORM:
E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
ICATION DATA:
N NUMBER: US/08/912,951
CE: 14-AUG-1997
ATION: 435
ATION DATA:
N NUMBER: US 08/854,050
CE: 09-MAY-1997
ATION: 435
ATION DATA:
N NUMBER: US 08/851,843

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; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-912-951-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;

Qy 1 MPRAPRCRAVRSLLRSHYREVLPVPLATFVRRLGPOGWRLVQRGDPAAFRALVAQCI
Db 1 MPRAPRCRAVRSLLRSHYREVLPVPLATFVRRLGPOGWRLVQRGDPAAFRALVAQCI
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Db 61 DARPPAAPSPRQVSCIKELVARVLQRLCERGANVLAFGFALLDGGARGGPEAI
Qy 121 SYLPTVTVDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPI
Db 121 SYLPTVTVDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPI
Qy 181 ATOARPPPHASGPRRLGRCERAMNHSVREAGVPLGLPAPGARRRGGGSASRLPLI
Db 181 ATOARPPPHASGPRRLGRCERAMNHSVREAGVPLGLPAPGARRRGGGSASRLPLI
Qy 241 GAAPERTPTVQGSWAHPQRTGRGSDRGFCVVSPPARPAEATSLGALSGRHI
Db 241 GAAPERTPTVQGSWAHPQRTGRGSDRGFCVVSPPARPAEATSLGALSGRHI
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Db 301 RQHAGPPTSRPPRPMWDTPCPPVYAKTKHFLYSSGDKBOLRPSFLLSLRPSLI
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Db 361 VETIFLGRSPWMPGTTPRLPRLPQRYWQMRPLFLELLGNHAQCQPYGVLLKTHCP
Qy 421 PAAGVCAREKPGQSVAAPEEEDTPRLVOLLRQHSPPWQYGFVRACLRLVPI
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRLVOLLRQHSPPWQYGFVRACLRLVPI
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Db 481 RHNERFLRNTKKFISLGKAKLSLQELTWKMSVRDCAWLRSPGVCVPAAEH
Qy 541 LAKFLHWMMSVYVVELLRSPFFYVTTTFFQKNRFFFYRKSVWSKLQSIGIRQLK
Db 541 LAKFLHWMMSVYVVELLRSPFFYVTTTFFQKNRFFFYRKSVWSKLQSIGIRQLK

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lication US/09402181B
 839

ATION:

I: Cech, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin B.
 Andrews, William H.
 INVENTION: Human Telomerase Catalytic Subunit
 F SEQUENCES: 633
 VENCE ADDRESS:
 RESSEE: Townsend and Townsend and Crew LLP
 SET: Two Embarcadero Center, Eighth Floor
 Y: San Francisco
 TE: California
 TRY: USA

: 94111-3834

READABLE FORM:

IUM TYPE: Floppy disk

UTER: IBM PC compatible

RATING SYSTEM: PC-DOS/MS-DOS

WARE: Patent in Release #1.0, Version #1.30

APPLICATION DATA:

PLICATION NUMBER: US/09/402,181B

ING DATE: 29-Sep-1997

SSIFICATION: <Unknown>

PLICATION DATA:

PLICATION NUMBER: US 08/724,643

ING DATE: 01-OCT-1996

PLICATION NUMBER: US 08/844,419

ING DATE: 18-APR-1997

ICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Ausenhus, Scott L.
 REGISTRATION NUMBER: 42,271
 REFERENCE/DOCKET NUMBER: 015389-002620US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1132 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-402-181B-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0;

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 DB 541 LAKFLHMLSVVVELLSRFFVYTTTQKNRLLFFYRKSVMKLSQISIGIRQLKR

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 TRHRTVYVPLGSLRTAQTOLSRKLPQTTLTALAAANPALPSDEKTIIL 1132

Application US/09721456
 7110
 INFORMATION:
 AT: Cech, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin B.
 Andrews, William H.
 ? INVENTION: Human Telomerase Catalytic Subunit
 OF SEQUENCES: 727
 DNDENCE ADDRESS:
 DRESSEE: Townsend and Townsend and Crew LLP
 RET: Two Embarcadero Center, Eighth Floor
 Y: San Francisco
 TE: California
 NTRY: USA
 P: 94111-3834
 3 READABLE FORM:
 IUM TYPE: Floppy disk
 PUTER: IBM PC compatible
 ERATING SYSTEM: PC-DOS/MS-DOS
 TWARE: Patent In Release #1.0, Version #1.30
 APPLICATION DATA:
 APPLICATION NUMBER: US/09/721,456
 LING DATE: 22-NOV-2000
 ASSIFICATION: <Unknown>
 APPLICATION DATA:
 APPLICATION NUMBER: US/08/974,549A
 LING DATE: 19-NOV-1997
 APPLICATION NUMBER: US 08/724,643
 LING DATE: 01-OCT-1996
 APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: WO PCT/US97/17618
 FILING DATE: 01-OCT-1997
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-0026100S
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1132 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-721-456-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0;

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 DB 1 MPRAPCRAVRSLLRSHYREVLPLATFVRRLGPOGWRLVQRGDDPAAPRALVAQC
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 DB 61 DARPPPAAPSPRQVSCLELVARVLQRLCERGAKNVLAFAFGALLDARGGPPPEA
 QY 121 SYLNTVTDALRGSGANGLLRLRVGDDVLVHLLARCALFVLVAPSCAYQVCGPP
 DB 121 SYLNTVTDALRGSGANGLLRLRVGDDVLVHLLARCALFVLVAPSCAYQVCGPP
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 DB 421 PAAGVCAREKPGQSVAAPEEDTDPRLVQLLRHSSPQVYGVFVRACLRLVPI
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 DB 481 RHNERFRRLNTKKFISLGKHAKLISLQELTWKMSVRDCAWLRRSPGVGCVPAAEH

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VHRVTVPLGSLRTAQTOLSRKLPCTTLTALAANAALPSPDFXTILD 1132

lication US/09953052

619

NATION:

T: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

INVENTION: Antisense Compositions for Detecting and
Inhibiting Telomerase Reverse Transcriptase

SEQUENCES: 72

NDENCE ADDRESS:

RESSEE: Townsend and Townsend and Crew LLP
EET: Two Embarcadero Center, Eighth Floor
Y: San Francisco
TE: California

NIRX: USA

94111-3834

READABLE FORM:

IUM TYPE: Floppy disk

PUTER: IBM PC compatible

RATING SYSTEM: PC-DOS/MS-DOS

TWARE: Patent In Release #1.0, Version #1.30

PLICATION DATA:

PLICATION NUMBER: US/09/953,052

ING DATE: 14-Sep-2001

SSIFICATION: <Unknown>

PLICATION DATA:

APPLICATION NUMBER: 09/052,919
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Amette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 015389-003600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-953-052-2

Query Match 100.0%; Score 5961; DB 4; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;
QY 1 MPRAPRCRAVRSLLRSHYREVLPVPLATFVRRLGPGQWELVQGDPAAFRALVAQCI
DB 1 MPRAPRCRAVRSLLRSHYREVLPVPLATFVRRLGPGQWELVQGDPAAFRALVAQCI
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1 Application US/08974549A

178

ATION:

Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

ENTION: Human Telomerase Catalytic Subunit

QUENCES: 727

ICE ADDRESS:

Townsend and Townsend and Crew LLP

Two Embarcadero Center, Eighth Floor

San Francisco

California

USA

1-3834

ADABLE FORM:

E: Floppy disk

IBM PC compatible

SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 611:
SEQUENCE CHARACTERISTICS:
LENGTH: 1154 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
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LOCATION: 1..1154
OTHER INFORMATION: /note= "fusion protein composed of hprt
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US-08-974-549A-611

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Best Local Similarity 100.0%; Pred. No. 0;
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1 APPLICANT: Chapman, Karen B.
2 APPLICANT: Morin, Gregg B.
3 APPLICANT: Harley, Calvin
4 APPLICANT: Andrews, William H.
5 TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGN
6 TITLE OF INVENTION: HUMANEUTROTIC METHODS
7 NUMBER OF SEQUENCES: 335
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Townsend and Townsend and Crew LLP
10 STREET: Two Embarcadero Center, 8th Floor
11 CITY: San Francisco
12 STATE: California
13 COUNTRY: United States of America
14 ZIP: 94111
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: PatentIn Release #1.0, Version #1.30
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/912,951
22 FILING DATE: 14-AUG-1997
23 CLASSIFICATION: 435
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 08/854,050
26 FILING DATE: 09-MAY-1997
27 CLASSIFICATION: 435
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: US 08/851,843
30 FILING DATE: 06-MAY-1997
31 CLASSIFICATION: 435
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34 FILING DATE: 25-APR-1997
35 CLASSIFICATION: 435
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38 FILING DATE: 18-APR-1997
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41 APPLICATION NUMBER: US 08/724,643
42 FILING DATE: 01-OCT-1996
43 CLASSIFICATION: 435
44 ATTORNEY/AGENT INFORMATION:
45 NAME: Apple, Randolph T.
46 REGISTRATION NUMBER: 36,429
47 REFERENCE/DOCKET NUMBER: 015389-002600US
48 TELECOMMUNICATION INFORMATION:
49 TELEPHONE: (415) 576-0200
50 TELEFAX: (415) 576-0300
51 INFORMATION FOR SEQ ID NO: 323:
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ATION:
Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru

Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Townsend and Townsend and Crew LLP
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

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APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>

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FILING DATE: 01-OCT-1996
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FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 611:
SEQUENCE CHARACTERISTICS:
LENGTH: 1154 amino acids
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GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;   Lingner, Joachim
;   Nakamura, Toru
;   Chapman, Karen B.
;   Morin, Gregg B.
;   Harley, Calvin B.
;   Andrews, William H.
;
TITLE OF INVENTION: Human telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
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; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
;
ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 013389-002610US
;
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
;
INFORMATION FOR SEQ ID NO: 611:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1154 amino acids
;   TYPE: amino acid
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US-09-424-686F-2

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Minimum Match 0%

Maximum Match 100%

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ALIGNMENTS

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; APPLICANT: Morlin, Gregg B.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
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; PRIOR FILING DATE: 1998-08-03
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US-09-990-080-2

Query Match 100.0%; Score 5961; DB 9; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;
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plication US/09749728B

020142457A1

TION:

zawa, Akihiro

ta, Jun-Ichi

kuda, Keiichi

zawa, Satoshi

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; APPLICANT: Sakurada, Kazuhiro
; APPLICANT: Gojo, Satoshi
; APPLICANT: Yamada, Yoji
; TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENT
; FILE REFERENCE: 00766.000043
; CURRENT APPLICATION NUMBER: US/09/749,728B
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: H11-372826
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: PCT-JP00-01148
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: PCT-JP00-07741
; PRIOR FILING DATE: 2000-11-02
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver.2.0
; SEQ ID NO 31
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-749-728B-31

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Query Match 100.0%; Score 5961; DB 9; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;

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Application US/09843676
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 MATION:
 T: Cech, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, Calvin
 Andrews, William H.
 INVENTION: NO. US20020164786A1 Telomerase
 F SEQUENCES: 225
 NDENCE ADDRESS:
 RESSEE: Townsend and Townsend and Crew LLP
 RET: Two Embarcadero Center, 8th Floor
 Y: San Francisco
 TE: California
 NTRY: United States of America
 : 94111
 READABLE FORM:
 IUM TYPE: Floppy disk
 PUTER: IBM PC compatible
 RATING SYSTEM: PC-DOS/MS-DOS
 TWARE: Patent In Release #1.0, Version #1.30
 APPLICATION DATA:
 APPLICATION NUMBER: US/09/843,676
 ING DATE: 26-Apr-2001
 ASSIFICATION: 536
 PPLICATION DATA:
 PPLICATION NUMBER: US/08/854,050
 ING DATE: 09-MAY-1997
 PPLICATION NUMBER: US 08/846,017
 ING DATE: 25-APR-1997
 PPLICATION NUMBER: US 08/844,419
 ING DATE: 18-APR-1997
 PPLICATION NUMBER: US 08/724,643
 ING DATE: 01-OCT-1996
 /AGENT INFORMATION:
 IE: Apple, Randolph T.
 ISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-0029300S
 MUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 225:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1132 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 225:
 US-09-843-676-225

Query Match 100.0%; Score 5961; DB 9; Length 1132;
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plication US/09953052
0020173476A1
EMATION:
NT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
F INVENTION: Antisense Compositions for Detecting and
Inhibiting Telomerase Reverse Transcriptase
OF SEQUENCES: 72
CNDESC ADDRESS:
DRESSER: Townsend and Townsend and Crew LLP
REBT: Two Embarcadero Center, Eighth Floor
TY: San Francisco
ATE: California
JNTRY: USA
P: 94111-3834
3 READABLE FORM:
DIUM TYPE: Floppy disk
MPTER: IBM PC compatible
ERATING SYSTEM: PC-DOS/MS-DOS
FTWARE: Patent In Release #1.0, Version #1.30
APPLICATION DATA:
PLICATION NUMBER: US/09/953,052
ING DATE: 14-Sep-2001
ASSIFICATION: <Unknown>
PLICATION DATA:
PLICATION NUMBER: 09/052,919
ING DATE: <Unknown>
PLICATION NUMBER: US 08/844,419
ING DATE: 18-APR-1997
PLICATION NUMBER: US 08/846,017
ING DATE: 25-APR-1997
PLICATION NUMBER: US 08/851,843
ING DATE: 06-MAY-1997
PLICATION NUMBER: US 08/854,050
ING DATE: 09-MAY-1997
PLICATION NUMBER: US 08/911,312
ING DATE: 14-AUG-1997
PLICATION NUMBER: US 08/912,951
ING DATE: 14-AUG-1997
PLICATION NUMBER: US 08/915,503
ING DATE: 14-AUG-1997
PLICATION NUMBER: US 08/974,549
ING DATE: 19-NOV-1997
PLICATION NUMBER: US 08/974,584
ING DATE: 19-NOV-1997
PLICATION NUMBER: WO PCT/US97/17618
ING DATE: 01-OCT-1997

APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 015389-0036000US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-953-052-2
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Matches 1132; Conservative 0; Mismatches 0; Indels 0;
QY 1 MPAPRCRAVRSLLRSHYREVLPATFVRRLPQGMRLVQRGDPAAFRALVAQC
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; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ausenhus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-0026200S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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; US-10-325-810-2

Query Match          100.0%; Score 5961; DB 12; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;

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 3FKAGRNMRKLFGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRPHACVQLP 1020
 QQWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
 QQWKNPTFFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLL 1080
 TRHRVTVPLLSGLRTAQTLQSRKLPQTTLTAAEAAANPALPSDFKTILD 1132
 TRHRVTVPLLSGLRTAQTLQSRKLPQTTLTAAEAAANPALPSDFKTILD 1132

plication US/10388578
 . US20030224411A1
 ATION:
 ron Corporation
 tanton, Lawrence
 alph, Brandenberger
 oseph, Gold D.
 chn, Irving
 andalam, Ramkumar
 ok, Michael
 helton, Dawne
 NTION: Genes that are Up- or Down-Regulated During Differentiation of Hu
 NTION: Embryonic Stem Cells
 E: 135/001
 CATION NUMBER: US/10/388,578
 G DATE: 2003-03-13
 ID NOS: 139
 tom

mo sapiens

ilarity 100.0%; Score 5961; DB 12; Length 1132;
 Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

RAPRCRAVRSLLRSHYREVLPLATFVRRLGPGQWRLVQRGDPAAFRALVAQCLVCVW 60
 RAPRCRAVRSLLRSHYREVLPLATFVRRLGPGQWRLVQRGDPAAFRALVAQCLVCVW 60
 RPPPAAPSFRVSCIKELVARVQLRCERGAKNVLAFGFALLDAGRGPPPEAFTTSVR 120
 RPPPAAPSFRVSCIKELVARVQLRCERGAKNVLAFGFALLDAGRGPPPEAFTTSVR 120
 LPNTVTDALRGSGWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 LPNTVTDALRGSGWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
 QARPPPHASGPRRLRCERANHSVREAGVPLGLPAPCARBRGSGASRSLPLPKRPRR 240
 QARPPPHASGPRRLRCERANHSVREAGVPLGLPAPGARRRGGSGASRSLPLPKRPRR 240

QY 241 GAAPEPERTVYQGSWAHPGTRGFSDRGFCVSPARPAEATISLEGALSCTRH
 DB 241 GAAPEPERTVYQGSWAHPGTRGFSDRGFCVSPARPAEATISLEGALSCTRH
 QY 301 ROHAGAPPSTSRPRPMDTPCPVYAEKHPFLYSSGDKQELRPSFLSSLRPSL
 DB 301 ROHAGAPPSTSRPRPMDTPCPVYAEKHPFLYSSGDKQELRPSFLSSLRPSL
 QY 361 VETIFLGSRPMWPGTPRRLPRLPORYWCMRPLFLELLGNHACQCPYGVLLKTHCP
 DB 361 VETIFLGSRPMWPGTPRRLPRLPORYWCMRPLFLELLGNHACQCPYGVLLKTHCP
 QY 421 PAAGVCAREKPGQSVAAPEEEDTDPRLVQLLRQHSSEPWQYVFRACLRRLVP
 DB 421 PAAGVCAREKPGQSVAAPEEEDTDPRLVQLLRQHSSEPWQYVFRACLRRLVP
 QY 481 RHNERFRUNTKKFTISLGKHAKLSIQLTWNMSVRDCAWLRSRSGVGVCPAAEH
 DB 481 RHNERFRUNTKKFTISLGKHAKLSIQLTWNMSVRDCAWLRSRSGVGVCPAAEH
 QY 541 LAKFLHMLMSVYVVELLRSFFVVTETTFQKNRLEFFYRKSVMKLSQSIGIRQHLK
 DB 541 LAKFLHMLMSVYVVELLRSFFVVTETTFQKNRLEFFYRKSVMKLSQSIGIRQHLK
 QY 601 LSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNMDYVVGARTFRREKRAERL
 DB 601 LSEAEVROHREARPAALLTSRLRFPKPDGLRPIVNMDYVVGARTFRREKRAERL
 QY 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRQAQDPPPELYFVKVDVT
 DB 661 LFSVLNYERARRPGLLGASVLGLDDIHRAWRTFVLVRQAQDPPPELYFVKVDVT
 QY 721 PQDRLETVIASIIKPNQTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLPYMR
 DB 721 PQDRLETVIASIIKPNQTYCVRRYAVVQAAHGHVRKAFKSHVSTLTDLPYMR
 QY 781 QETSPLRDAVIEQSSSLNEASSGLFDVFLRPMCHHVRIRGKSVYQCGIPQG
 DB 781 QETSPLRDAVIEQSSSLNEASSGLFDVFLRPMCHHVRIRGKSVYQCGIPQG
 QY 841 LCSLCYGDWENKLFAGIRDRDGLLLRLVDDFLVTPHLLTHAKTFLRVLRGVPEY
 DB 841 LCSLCYGDWENKLFAGIRDRDGLLLRLVDDFLVTPHLLTHAKTFLRVLRGVPEY
 QY 901 RKTVVNFPVEDEALGCTAFVQMPAHGLFPWCGLLLDTRTLEVSQSYSSYARTSI
 DB 901 RKTVVNFPVEDEALGCTAFVQMPAHGLFPWCGLLLDTRTLEVSQSYSSYARTSI
 QY 961 NRGFKAGRNMRKLFGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRPHA
 DB 961 NRGFKAGRNMRKLFGLRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRPHA
 QY 1021 FHQOYWKNPTEFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLC
 DB 1021 FHQOYWKNPTEFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLC
 QY 1081 KLTRHRVTVPLLSGLRTAQTLQSRKLPQTTLTAAEAAANPALPSDFKTILD 1
 DB 1081 KLTRHRVTVPLLSGLRTAQTLQSRKLPQTTLTAAEAAANPALPSDFKTILD 1

RESULT 7

US-10-053-758-225
 ; Sequence 225, Application US/10053758
 ; Publication No. US20030032075A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cech, Thomas R.
 ; Lingner, Joachim
 ; Nakamura, Toru
 ; Chapman, Karen B.
 ; Morin, Gregg B.
 ; Harley, Calvin

us-09-424-686f-2.rapb

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100.0%; Score 5961; DB 14; Length 1132;
arity 100.0%; Pred. No. 0;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

JAPRCVAVSLLSRSHYREVLPLATFVRRLLGPGQWRLVQRGDDPAAPRALVAQCLVCVPW 60
JAPRCVAVSLLSRSHYREVLPLATFVRRLLGPGQWRLVQRGDDPAAPRALVAQCLVCVPW 60
JAPRCVAVSLLSRSHYREVLPLATFVRRLLGPGQWRLVQRGDDPAAPRALVAQCLVCVPW 60
JPPAAPSPQVSCLEKELVARVLQRLCERGAKNVLAFGFALLDARGGPEAFTTSVR 120
JPPAAPSPQVSCLEKELVARVLQRLCERGAKNVLAFGFALLDARGGPEAFTTSVR 120
JNTVTDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
JNTVTDALRGSGAWGLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
JAPPPHAGSPRRRLCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRRR 240
JAPPPHAGSPRRRLCERAWNHSVREAGVPLGLPAPGARRRGGSASRSLPLPKRRR 240
JPEPERTPVQGSWAHPGTRGSDRGFCVVSFAPPAEATSLLEGALSGTRHSHPSVG 300
JPEPERTPVQGSWAHPGTRGSDRGFCVVSFAPPAEATSLLEGALSGTRHSHPSVG 300
JHAGPSTGRPPRPMTWPCPPVYAETHKFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360
JHAGPSTGRPPRPMTWPCPPVYAETHKFLYSSGDKEQLRPSFLLSSLRPSLTGARRL 360

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entIn Ver. 2.0

no sapiens

100.0%; Score 5961; DB 14; Length 1132;
ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RAPCRVRSLLRSHYEVLPATFVRRRLPQGHRLVORGDPAAFRALVAQCLVCVPM 60
RAPCRVRSLLRSHYEVLPATFVRRRLPQGHRLVORGDPAAFRALVAQCLVCVPM 60
RPPPAAPSFROVSCLELVARVLCERGAONVLAFGFALLDARGGPPPEAFTTSVR 120
RPPPAAPSFROVSCLELVARVLCERGAONVLAFGFALLDARGGPPPEAFTTSVR 120
LPNTVTDALRGSGAWGLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
LPNTVTDALRGSGAWGLLRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPPLYQLGA 180
QARPPPHASGPRRLGGERAWNHVSREAGVPLGLPAGARRRGSGASRSLLPKRPR 240
QARPPPHASGPRRLGGERAWNHVSREAGVPLGLPAGARRRGSGASRSLLPKRPR 240
APEPERTPVGGGWAHPRTRGSDRGFCVVSPPARPAEATSLEGALSGTRHSHPSVG 300
APEPERTPVGGGWAHPRTRGSDRGFCVVSPPARPAEATSLEGALSGTRHSHPSVG 300
HHAGPPSTSRPPRMDTPCPVYAEKHFYSSGDKQLRPSFLLSRLPSLTGARLL 360
HHAGPPSTSRPPRMDTPCPVYAEKHFYSSGDKQLRPSFLLSRLPSLTGARLL 360
TIFLGSPPMPCGTRRLPLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
TIFLGSPPMPCGTRRLPLPQRYWQMRPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
AGVCAREKPGQSVAAPEEDTDPRLLVQLRHSSPMQVGFVRACLRRLVPPGLMGS 480
AGVCAREKPGQSVAAPEEDTDPRLLVQLRHSSPMQVGFVRACLRRLVPPGLMGS 480
NERFLRNTKXFI SLGHAKLSLOELTWKMSVRDCAMLRSPGVGCVPAAEHRLREI 540
NERFLRNTKXFI SLGHAKLSLOELTWKMSVRDCAMLRSPGVGCVPAAEHRLREI 540
KFLHLMASVYVVELLSRFFYVTTETFOKNRLFYFKSVWSKLSQIGIRQHLKRVOLRE 600
KFLHLMASVYVVELLSRFFYVTTETFOKNRLFYFKSVWSKLSQIGIRQHLKRVOLRE 600
EAEVROHREARPAALTSRLRIPKPDGLRPIVNDYVVGARTFRREKRAERLTSRVKA 660
EAEVROHREARPAALTSRLRIPKPDGLRPIVNDYVVGARTFRREKRAERLTSRVKA 660
SVLNYERARRPGLIGASVLGDDIHRARWTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
SVLNYERARRPGLIGASVLGDDIHRARWTFVLRVRAQDPPPELYFVKVDVTGAYDTI 720
IDLTEVIASIIKPNQTYCVRYAVVQKAAGHVRAKAFKSHVSTLTDLPYMRQVFAHL 780
IDLTEVIASIIKPNQTYCVRYAVVQKAAGHVRAKAFKSHVSTLTDLPYMRQVFAHL 780
TSPLRDAVVEIOSLSNEASSGLFDVFLRFMCHAVIRGKSYVQCQIPGOSTLSTL 840
TSPLRDAVVEIOSLSNEASSGLFDVFLRFMCHAVIRGKSYVQCQIPGOSTLSTL 840
SLCYGDMENKUFAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRLVRGVPYGCVMNL 900
SLCYGDMENKUFAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRLVRGVPYGCVMNL 900
TVVNEPVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSLTF 960

Db 901 RKTVVNFVEDEALGGTAFVQMPAHGLFPWCGLLDTRTLEVSQSDYSYARTSI
QY 961 NRGFKAGNMRKLFGLVRLKCHSLFLDLQVNSLQVCTNIYKILLQAYRPHA
Db 961 NRGFKAGNMRKLFGLVRLKCHSLFLDLQVNSLQVCTNIYKILLQAYRPHA
QY 1021 FHQQVWKNPTFFLRVISDASLCYSILKAKNAGMSLGAKGAGPLPSEAVOWLC
Db 1021 FHQQVWKNPTFFLRVISDASLCYSILKAKNAGMSLGAKGAGPLPSEAVOWLC
QY 1081 KLTRHRVTYVPLLSLRTAQTOLSKLPGTTLTALAAANPALPSDFKTILD 1
Db 1081 KLTRHRVTYVPLLSLRTAQTOLSKLPGTTLTALAAANPALPSDFKTILD 1

RESULT 9

US-10-054-295-225
; Sequence 225, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: NO. US20030044953A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 225:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 225:
US-10-054-295-225

Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;

Qy	1081	KLTRHRTVTVPLIGSLRTAQTLQSRKLPQTTTALFAAANPALPSDFKTLTD	
Db	1081	KLTRHRTVTVPLIGSLRTAQTLQSRKLPQTTTALFAAANPALPSDFKTLTD	
RESULT 10			
US-10-054-611-225			
Sequence 225, Application US/10054611			
Publication No. US20030059787A1			
GENERAL INFORMATION:			
APPLICANT: Cech, Thomas R.			
Lingner, Joachim			
Nakamura, Toru			
Chapman, Karen B.			
Morin, Gregg B.			
Harley, Calvin			
Andrews, William H.			
TITLE OF INVENTION: No. US20030059787A1el Telomerase			
NUMBER OF SEQUENCES: 225			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Townsend and Townsend and Crew LLP			
STREET: Two Embarcadero Center, 8th Floor			
CITY: San Francisco			
STATE: California			
COUNTRY: United States of America			
ZIP: 94111			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patent In Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/10/054,611			
FILING DATE: 18-Jan-2002			
CLASSIFICATION: 536			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: 08/854,050			
FILING DATE: <Unknown>			
APPLICATION NUMBER: US 08/846,017			
FILING DATE: 25-APR-1997			
APPLICATION NUMBER: US 08/844,419			
FILING DATE: 18-APR-1997			
APPLICATION NUMBER: US 08/724,643			
FILING DATE: 01-OCT-1996			
ATTORNEY/AGENT INFORMATION:			
NAME: Apple, Randolph T.			
REGISTRATION NUMBER: 36,429			
REFERENCE/DOCKET NUMBER: 015389-002930US			
TELEPHONE: (415) 576-0200			
TELEFAX: (415) 576-0300			
INFORMATION FOR SEQ ID NO: 225:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 1132 amino acids			
TYPE: amino acid			
TOPOLOGY: linear			
MOLECULE TYPE: protein			
SEQUENCE DESCRIPTION: SEQ ID NO: 225:			
US-10-054-611-225			
Query Match	100.0%;	Score 5961;	DB 14; Length 1132;
Best Local Similarity	100.0%;	Pred. No. 0;	
Matches 1132;	Conservative 0;	Mismatches 0;	Indels 0;
Qy	1	MPRAPRCRAVRSLLRSHYREVLFPLATFVRRLGQWRLVQRGDPAAPRALVAQC	
Db	1	MPRAPRCRAVRSLLRSHYREVLFPLATFVRRLGQWRLVQRGDPAAPRALVAQC	
Qy	61	DARPPPAAPSFQVSCLELVARVLQRLCERGAQNLVAFGALLDGAAGGPPFA	
Db	61	DARPPPAAPSFQVSCLELVARVLQRLCERGAQNLVAFGALLDGAAGGPPFA	
Qy	121	SVLPNTVTYDALRGSGAGMGLRRVGDVIVHLLARCALFVLVAPSCAYOVCVGP	

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LPNTVTDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYLGA 180
QARPPPHASGRRRLGGERANWHSVREAGVPLGLPAPGARRRGGASASLSLPPKRR 240
QARPPPHASGRRRLGGERANWHSVREAGVPLGLPAPGARRRGGASASLSLPPKRR 240
JAEPEPTVGGQSWAHPGRTGRPSDRGFCVVSAPARAEATSLGALSGTRSHPSVG 300
JAEPEPTVGGQSWAHPGRTGRPSDRGFCVVSAPARAEATSLGALSGTRSHPSVG 300
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JHAGPSTSRPPRPWDTPCPVVAETKHFLYSSGDKQLRPSFLLSSLRPSLTGARRL 360
TIFLGRSPWMPCTPRRLPRLPORYWQMPPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
TIFLGRSPWMPCTPRRLPRLPORYWQMPPLFLELLGNHAQCPYGVLLKTHCPRAAVT 420
JAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSSPMQVYGFVRACLRLVPPGLWGS 480
JAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSSPMQVYGFVRACLRLVPPGLWGS 480
INERFLRNTKKFISLGKHAKLLOELTWKMSVRDCAMLRSPGVCVPAAEHRLREEI 540
INERFLRNTKKFISLGKHAKLLOELTWKMSVRDCAMLRSPGVCVPAAEHRLREEI 540
KFLHLMMSVYVVELLSRFYVTTETTFQKNRLFYFRKSVWSKLSQSIGIRHKLKVQRE 600
KFLHLMMSVYVVELLSRFYVTTETTFQKNRLFYFRKSVWSKLSQSIGIRHKLKVQRE 600
JBAEVQHREARPAULTSLRFLPKPDGLRPIVNDYVVGARTFREKKAERLTSRKVA 660
JBAEVQHREARPAULTSLRFLPKPDGLRPIVNDYVVGARTFREKKAERLTSRKVA 660
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SVLNYERARRPGLLGASVLGLDDIHRARWTFVLVRADQPPPELYFVKVDTGYADTI 720
JRLTEVIASIIKPNQTYCVRVAVVQKAAHGHVRKAFKSHVSTLTDLOPYMRQFVAHL 780
JRLTEVIASIIKPNQTYCVRVAVVQKAAHGHVRKAFKSHVSTLTDLOPYMRQFVAHL 780
TSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYQCQGIPOGSIILSTL 840
TSPLRDAVVIQSSSLNEASSGLFDVFLRFMCHHAVIRGKSVYQCQGIPOGSIILSTL 840
SLCYGDMENKLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYGCWNL 900
SLCYGDMENKLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRTLVRGVPYGCWNL 900
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JGFKAGNNRRKLFGLVRLKCHSLFDLQVNSLQTVCTNIYKILLQAVRFHACVQLP 1020
JGFKAGNNRRKLFGLVRLKCHSLFDLQVNSLQTVCTNIYKILLQAVRFHACVQLP 1020
JQVWKNPTFFLRVSDTASLCYSILKAKNAGNSLGAKAGPLPSEAVQWILCHOAFL 1080
JQVWKNPTFFLRVSDTASLCYSILKAKNAGNSLGAKAGPLPSEAVQWILCHOAFL 1080
JTHRVYVYPLGLSLRTAOTQLSRKLPGTTLTALEAANPALPSPDKFTILD 1132
JTHRVYVYPLGLSLRTAOTQLSRKLPGTTLTALEAANPALPSPDKFTILD 1132

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application US/10105963
 2. US20030068818A1
 ACTION:

```

; APPLICANT: Geron Corporation
; APPLICANT: Denning, Chris
; APPLICANT: Clark, A. John
; APPLICANT: Schiff, J. Michael
; TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Comi
; TITLE OF INVENTION: Transplantation and a Carbohydrate Determina
; FILE OF INVENTION: Recombination
; FILE OF INVENTION: 731/002
; CURRENT APPLICATION NUMBER: US/10/105,963
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/277,811
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1132
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-105-963-2

Query Match 100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;

QY 1 MPRAPCRVAVRSLLSRSHYREVLPATFVRRLLPGQWRLVQRGDPAAFRALVAQC
Db 1 MPRAPCRVAVRSLLSRSHYREVLPATFVRRLLPGQWRLVQRGDPAAFRALVAQC
QY 61 DARPPAAASFPQVSCLELVARVLQRLCERGAKNVLAFAEALLDGCAGGPPF
Db 61 DARPPAAASFPQVSCLELVARVLQRLCERGAKNVLAFAEALLDGCAGGPPF
QY 121 SYLNTNTVDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPE
Db 121 SYLNTNTVDALRGSGAWGLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPE
QY 181 ATQARPPPHASGRRRLGGERANWHSVREAGVPLGLPAPGARRRGGASASLSPI
Db 181 ATQARPPPHASGRRRLGGERANWHSVREAGVPLGLPAPGARRRGGASASLSPI
QY 241 GAPEPERTVPGQSWAHPGRTGRPSDRGFCVVSAPARAEATSLGALSGTR
Db 241 GAPEPERTVPGQSWAHPGRTGRPSDRGFCVVSAPARAEATSLGALSGTR
QY 301 RQHAGPPSTSRPPRPWDTPCPVVAETKHFLYSSGDKQLRPSFLLSSLRPSI
Db 301 RQHAGPPSTSRPPRPWDTPCPVVAETKHFLYSSGDKQLRPSFLLSSLRPSI
QY 361 VETIFLGRSPWMPCTPRRLPRLPORYWQMPPLFLELLGNHAQCPYGVLLKTHCI
Db 361 VETIFLGRSPWMPCTPRRLPRLPORYWQMPPLFLELLGNHAQCPYGVLLKTHCI
QY 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSSPMQVYGFVRACLRLVI
Db 421 PAAGVCAREKPGQSVAAPEEEDTPRRLVQLLRQHSSPMQVYGFVRACLRLVI
QY 481 RHNERFLRNTKKFISLGKHAKLLOELTWKMSVRDCAMLRSPGVCVPAAE
Db 481 RHNERFLRNTKKFISLGKHAKLLOELTWKMSVRDCAMLRSPGVCVPAAE
QY 541 LAKFLHLMMSVYVVELLSRFYVTTETTFQKNRLFYFRKSVWSKLSQSIGIRHKL
Db 541 LAKFLHLMMSVYVVELLSRFYVTTETTFQKNRLFYFRKSVWSKLSQSIGIRHKL
QY 601 LSAEAVRQHREARPAULTSLRFLPKPDGLRPIVNDYVVGARTFREKKAERI
Db 601 LSAEAVRQHREARPAULTSLRFLPKPDGLRPIVNDYVVGARTFREKKAERI
QY 661 LFSVLNYERARRPGLLGASVLGLDDIHRARWTFVLVRADQPPPELYFVKVDVT
Db 661 LFSVLNYERARRPGLLGASVLGLDDIHRARWTFVLVRADQPPPELYFVKVDVT
QY 721 PQDRLTEVIASIIKPNQTYCVRVAVVQKAAHGHVRKAFKSHVSTLTDLOPYME

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RLTEVIASIIKQNTYCVRRYAVQKAAHGHVRKAFKSHVSTLTDLPVMRQFVAHL 780
|SPLRDVAVIEQSSSINEASSGLFDVFLRPMCHHAVIRKGSYVQCGIPQSSILSTL 840
|SPLRDVAVIEQSSSINEASSGLFDVFLRPMCHHAVIRKGSYVQCGIPQSSILSTL 840
|LCYGMENKLPAGIRRDGILLRLVDVFLVTPHLTHAKTFLRLTVRGVPEYGCVVNL 900
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|VNVFVDEALGCTAFVQMPAHGLFPWCGLLDLTDRTLEVQSDYSYVARTSIRASLT 960
|VNVFVDEALGCTAFVQMPAHGLFPWCGLLDLTDRTLEVQSDYSYVARTSIRASLT 960
|FKAGNRMRKLFGLVRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVQLQP 1020
|FKAGNRMRKLFGLVRLKCHSLFDLQVNSLQTVCTNIYKILLQAYRFHACVQLQP 1020
|QWKNPTFLRLVISTASLCYILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080
|QWKNPTFLRLVISTASLCYILKAKNAGMSLGAKGAGPLPSEAVQMLCHQAFLL 1080
|FHRVTYVPLLSRLTAQTLSRLKPLGTTTLTALEAANPALPSDFKTIID 1132
|FHRVTYVPLLSRLTAQTLSRLKPLGTTTLTALEAANPALPSDFKTIID 1132

Publication US/10044692
US20030096344A1
INVENTOR:
  Cecch, Thomas R.
  Lingner, Joachim
  Nakamura, Toru
  Chapman, Karen B.
  Morin, Gregg B.
  Harley, Calvin
  Andrews, William H.
INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
OF SEQUENCES: 335
SEQUENCE ADDRESS:
  DRESSEE: Townsend and Towneend and Crew LLP
  REF: Two Embarcadero Center, 8th Floor
  CITY: San Francisco
  STATE: California
  COUNTRY: United States of America
  P: 94111
  READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: Patent In Release #1.0, Version #1.30
  APPLICATION DATA:
  APPLICATION NUMBER: US/10/044,692
  FILING DATE: 11-Jan-2002
  ASSIGNMENT: <Unknown>
  APPLICATION DATA:
  APPLICATION NUMBER: 08/912,951
  FILING DATE: <Unknown>
  APPLICATION NUMBER: US 08/854,050
  FILING DATE: 09-MAY-1997
  APPLICATION NUMBER: US 08/851,843
  FILING DATE: 06-MAY-1997
  APPLICATION NUMBER: US 08/846,017
  FILING DATE: 25-APR-1997
  APPLICATION NUMBER: US 08/844,419
  FILING DATE: 18-APR-1997
  APPLICATION NUMBER: US 08/724,643
  FILING DATE: 01-OCT-1996
  AGENT INFORMATION:

```

```

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-00260005
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 576-0200
  TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 1132 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
    MOLECULE TYPE: protein
  SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-044-692-2

Query Match      100.0%; Score 5961; DB 14; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1132; Conservative 0; Mismatches 0; Indels 0;

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DB 61 DARPPPAAPSPQVSCLEKELVARVLQRLCERGAKNVLAFGFALLDGGARGGPEA
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DB 661 LFSVLNYERARPPGLIGASVLGLDDIHRAWETFLVRAQODPPPELYPVKVDVT
QY 721 PODRLTEVIASIIKQNTYCVRRYAVQKAAHGHVRKAFKSHVSTLTDLPYMR
DB 721 PODRLTEVIASIIKQNTYCVRRYAVQKAAHGHVRKAFKSHVSTLTDLPYMR
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plication US/10044539

US20030100093A1

RMATION:

NT: Cecch, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin

Andrews, William H.

INVENTION: HUMAN TSELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND

TERAPEUTIC METHODS

OF SEQUENCES: 335

ONDNCE ADDRESS:

DRESSEE: Townsend and Townsend and Crew LLP

REET: Two Embarcadero Center, 8th Floor

TY: San Francisco

ARE: California

UNTRY: United States of America

P: 94111

R READABLE FORM:

DUM TYPE: Floppy disk

MUTER: IBM PC compatible

ERATING SYSTEM: PC-DOS/MS-DOS

FTWARE: Patent In Release #1.0, Version #1.30

PLICATION DATA:

PLICATION NUMBER: US/10/044,539

LING DATE: 11-Jan-2002

ASSIFICATION: 435

PLICATION DATA:

PLICATION NUMBER: 08/912,951

LING DATE: <Unknown>

PLICATION NUMBER: US 08/854,050

LING DATE: 09-MAY-1997

PLICATION NUMBER: US 08/851,843

LING DATE: 06-MAY-1997

PLICATION NUMBER: US 08/846,017

LING DATE: 25-APR-1997

PLICATION NUMBER: US 08/844,419

LING DATE: 18-APR-1997

PLICATION NUMBER: US 08/724,643

LING DATE: 01-OCT-1996

Y/AGENT INFORMATION:

ME: Apple, Randolph T.

GISTRATION NUMBER: 36,429

PERENCE/DOCKET NUMBER: 015389-002600US

MUNICATION INFORMATION:

LEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1132 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-044-539-2
 Query Match 100.0%; Score 5961; DB 14; Length 1132;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1132; Conservative 0; Mismatches 0; Indels 0;
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 DB 1 MPAPRCRAVRSLLSHYREVLPATFVRRLGPOGWRLVORGDPAAFRALVAQC
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 DB 61 DARPPAAPSPFQVSCLEKELVARVLQRLCERCAKNVLAFFGALLDGAAGPPEA
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plication US/10295681

US20030166270A1

TION:

Premkumar Reddy

shil G. Rane

chard V. Mettus

TION: COMPOSITIONS AND METHODS FOR REVERSIBLY

TION: INDUCING CONTINUAL GROWTH IN NORMAL CELLS

: 6056-307

ATION NUMBER: US/10/295.681

DATE: 2002-11-15

ION NUMBER: US 60/334,760

ATE: 2001-11-15

ID NOS: 69

SEQ for Windows Version 4.0

io sapiens

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 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15

US-10-325-810-611

; Sequence 611, Application US/10325810

; Publication No. US20030204069A1

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin B.

; Andrews, William H.

; TITLE OF INVENTION: Human Telomerase Catalytic Subunit

; NUMBER OF SEQUENCES: 633

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

ERATING SYSTEM: PC-DOS/MS-DOS
 FWARE: Patent Release #1.0, Version #1.30

APPLICATION DATA:

PLICATION NUMBER: US/10/325,810

LING DATE: 20-Dec-2002

ASSIFICATION: <Unknown>

PLICATION DATA:

PLICATION NUMBER: US/09/402,181

LING DATE: 29-Sep-1997

PLICATION NUMBER: US/08/724,643

LING DATE: 01-OCT-1996

PLICATION NUMBER: US/08/844,419

LING DATE: 18-APR-1997

PLICATION NUMBER: US/08/846,017

LING DATE: 25-APR-1997

PLICATION NUMBER: US/08/851,843

LING DATE: 06-MAY-1997

PLICATION NUMBER: US/08/854,050

LING DATE: 09-MAY-1997

PLICATION NUMBER: US/08/911,312

LING DATE: 14-AUG-1997

PLICATION NUMBER: US/08/912,951

LING DATE: 14-AUG-1997

PLICATION NUMBER: US/08/915,503

LING DATE: 14-AUG-1997

PLICATION NUMBER: WO PCT/US97/17885

LING DATE: 01-OCT-1997

Y/AGENT INFORMATION:

4E: Ausenhus, Scott L.

3ISTRATION NUMBER: 42,271

ERENCE/DOCKET NUMBER: 015389-002620US

UNICATION INFORMATION:

PHONE: (415) 576-0200

EFAX: (415) 576-0300

FOR SEQ ID NO: 611:

3 CHARACTERISTICS:

NGTH: 1154 amino acids

PE: amino acid

RANDEDNESS: <unknown>

POLOGY: linear

3 TYPE: protein

4E/KEY: Protein

ATION: 1..1154

IER INFORMATION: /note= "fusion protein composed of hTERT

tein sequence, vector sequences, the

epitope and His6 tag"

3 DESCRIPTION: SEQ ID NO: 611:

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 ilarity 100.0%; Pred. No. 0;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 721 PODRLTEVIASIIKPONTYCVRRYAVVQKAHGHVRAKFKSHVSTLTLQPYMR
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 QY 841 LCSLCYGDENKLPAGIRRDGLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEY
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Search completed: April 22, 2004, 00:23:55
 Job time : 359 secs

GenCore version 5.1.6
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tein search, using sw model

April 21, 2004, 23:46:16 ; Search time 30 Seconds
(without alignments)
3629.627 Million cell updates/sec

US-09-424-686f-2

1 MPRAPRCRAVRSLLRSHYRE.....TALEAAANPALPSDFKTLID 1132

BLOSUM62

Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues

hits satisfying chosen parameters: 283366

length: 0
length: 2000000000

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 78:.*
1: piri:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

is the number of results predicted by chance to have a
ter than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

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6.1	1117	2	T14891		telomerase (EC 2.7
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3.0	3530	2	A59266		unconventional myo
2.9	660	1	Q0B23		BHLFI protein - hu
2.4	3511	2	A59295		unconventional myo
2.4	1560	2	T00080		hypothetical prote
2.4	1892	2	T18114		hypothetical prote
2.3	1460	1	EDBEIF		immediate-early pr
2.3	552	2	F75311		ABC transporter, A
2.3	924	2	S27923		gene LE3 protein -
2.3	1356	1	C45219		N-methyl-D-asparta
2.3	946	2	JC7810		inositol 1,4,5-tri
2.2	606	2	G75302		orotidine 5'-phosp
2.2	1106	2	JQ0405		hypothetical 119.5
2.2	860	2	S55543		RNA-directed DNA p
2.2	1184	2	G01763		atrophin-1 - human
2.2	1446	1	A45344		immediate-early pr
2.2	1184	2	S50832		atrophin-1 - human
2.2	2715	2	T13049		eyeid - fruit fly
2.2	383	2	S32975		gene BCRF2 protein
2.2	403	2	S52796		prip2 protein - hu
2.2	1776	2	G86280		protein T5821.13 [
2.2	628	2	S01955		hypothetical prote
2.1	376	2	C75580		adenine deaminase
2.1	1048	2	T31425		C-terminal domain-

proline-
actin-dej
probable
mixed-11
hypothet
hypothet
probable
transpos
pol prot
wiskott-
wiskott-
viral pr
tenascin
immediat
N-methyl
hypothet:

ALIGNMENTS

RESULT 1

T03844

telomerase catalytic chain - human

N;Alternate names: telomerase reverse transcriptase

C;Species: Homo sapiens (man)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-
C;Accession: T03844

R;Nakamura, T.M.; Morin, G.B.; Chapman, K.B.; Weinrich, S.L.; Andre
Science 277, 955-959, 1997

A;Title: Telomerase catalytic subunit homologs from fission yeast ar

A;Reference number: Z15111; MUID:97400623; PMID:9252327

A;Accession: T03844

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1132 <NAK>

A;Cross-references: EMBL:AF015950; NID:g2330016; PIDN:AAC51672.1; P1

A;Experimental source: kidney

C;Genetics:

A;Gene: TRF

A;Map position: 5p

Query	Match	Best Local Similarity	Score	5961;	DB 2;	Length	1132;
		100.0%;	100.0%;	Pred No. 0;	Mismatches	0;	Indels
QY	1	MPRAPRCRAVRSLLRSHYREVLPLATFVRLGFGQWRLVQRGDPAAFRALVAQC					
DB	1	MPRAPRCRAVRSLLRSHYREVLPLATFVRLGFGQWRLVQRGDPAAFRALVAQC					
QY	61	DARPPPAAPSFQVSCLELVARVLOLRCERGAKNVLAEPFALLDARGGPPPEI					
DB	61	DARPPPAAPSFQVSCLELVARVLOLRCERGAKNVLAEPFALLDARGGPPPEI					
QY	121	SYLPTNTVDALRGSGAWGLLRVGDVLLVHLLARCALFVLVAPSCAYQVCGPE					
DB	121	SYLPTNTVDALRGSGAWGLLRVGDVLLVHLLARCALFVLVAPSCAYQVCGPE					
QY	181	ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAPGARRRGGSSASRLPI					
DB	181	ATQARPPPHASGPRRLGGERAWNHSVREAGVPLGLPAPGARRRGGSSASRLPI					
QY	241	GAAPPEPTPVQGSWAHPGTRGSDRGFCVVSAPAEATSLGALSGRTRH					
DB	241	GAAPPEPTPVQGSWAHPGTRGSDRGFCVVSAPAEATSLGALSGRTRH					
QY	301	ROHAGAPPSTSPRPMDTPCPVVAETKHFYSSGDKEQLRPSFLLSSLRPSL					
DB	301	ROHAGAPPSTSPRPMDTPCPVVAETKHFYSSGDKEQLRPSFLLSSLRPSL					
QY	361	VTETIFLGRPMWPGTPRLPRLPQRYWQMRPLFLELLGNHAQCPCPYGVLLKTHCP					
DB	361	VTETIFLGRPMWPGTPRLPRLPQRYWQMRPLFLELLGNHAQCPCPYGVLLKTHCP					

AGVCAREKPGQSVAAPEBEDTDPRRLVQLLRQHSPPQVYGFVRACLRLVPPGLWGS 480
 |||||
 AGVCAREKPGQSVAAPEBEDTDPRRLVQLLRQHSPPQVYGFVRACLRLVPPGLWGS 480
 |||||
 INRRFLRNTKPIISLGKIAKLSLOELTWKMSVRDCAMLRSPGVCVPAABHRLREEI 540
 |||||
 INRRFLRNTKPIISLGKIAKLSLOELTWKMSVRDCAMLRSPGVCVPAABHRLREEI 540
 |||||
 KFLHLMWSVYVVELLSRSPFYVTEFTFQKNRLLFFYKRSVMSKLSQIGIRHKLRYQLRE 600
 |||||
 KFLHLMWSVYVVELLSRSPFYVTEFTFQKNRLLFFYKRSVMSKLSQIGIRHKLRYQLRE 600
 |||||
 EAEVRQHEARPAALLTSRLRIPKPDGLRPVNMVYVVGARTFRREKAEALTSRVKA 660
 |||||
 EAEVRQHEARPAALLTSRLRIPKPDGLRPVNMVYVVGARTFRREKAEALTSRVKA 660
 |||||
 SVLNYERARRRGLLGASVLGDDTHRAWRTPVLRVRAQDPPPELYFVKVQVGTAYDTI 720
 |||||
 SVLNYERARRRGLLGASVLGDDTHRAWRTPVLRVRAQDPPPELYFVKVQVGTAYDTI 720
 |||||
 DRLTEVIASIIKPNQTYCVRYAVVQKAAHGHVRKAFKSHYSTLTDLQPMRQFVAHL 780
 |||||
 DRLTEVIASIIKPNQTYCVRYAVVQKAAHGHVRKAFKSHYSTLTDLQPMRQFVAHL 780
 |||||
 TSPLRDVAVIBQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCQIGIPQGSILSTL 840
 |||||
 TSPLRDVAVIBQSSSLNEASSGLFDVFLRFMCHHAVIRGKSYVQCQIGIPQGSILSTL 840
 |||||
 SLCYGDMENKLFAGIRRGILLRLVDVLLVTPHLTHAKTFLRLVGRVPGVGVNL 900
 |||||
 SLCYGDMENKLFAGIRRGILLRLVDVLLVTPHLTHAKTFLRLVGRVPGVGVNL 900
 |||||
 TVNVPFVEDEALGTTAFVQMPAHGLFPMCGLLDTRTLEVOQSDYSYVARTSIRASLTF 960
 |||||
 TVNVPFVEDEALGTTAFVQMPAHGLFPMCGLLDTRTLEVOQSDYSYVARTSIRASLTF 960
 |||||
 GFKAQRNMRRKLFGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
 |||||
 GFKAQRNMRRKLFGLRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLP 1020
 |||||
 QQWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKAGPLPSEAVQWLCHOAFLL 1080
 |||||
 QQWKNPTFFLRVISTASLCYSILKAKNAGMSLGAKAGPLPSEAVQWLCHOAFLL 1080
 |||||
 TRHRVTVPILGSLRTAQTLQSRKLPGLTTLTALEAANPALPSPDFKTILD 1132
 |||||
 TRHRVTVPILGSLRTAQTLQSRKLPGLTTLTALEAANPALPSPDFKTILD 1132
 |||||

se transcriptase - Arabidopsis thaliana

g: protein F5E19_190

dopsis thaliana (mouse-ear cress)

000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000

517

mura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew

Protein Sequence Database, August 2000

er: Z25394

517

inary

DNA

23 <SAT>

es: EMBL:AL391147

ource: cultivar Columbia; BAC clone F5E19

5

0

125/3; 147/3; 185/1; 300/3; 325/1; 369/2; 414/3; 765/3; 942/2; 1033/2

12.2%; Score 724.5; DB 2; Length 1123;

ilarity 23.8%; Pred. No. 1e-41;

Matches 294; Conservative 199; Mismatches 511; Indels 233;
 QY 1 MPRAPRCRAVRSILRSHRYEVLPATFV-----RRLGPQGW-
 |||||
 Db 1 MPRKPRHYPELIMRLFGNRAENLDAIVDLIPNRNIQPCRCRCQGCGIGCS
 |||||
 QY 39 VQGGPAAAFRALVAOCLVCVPMADARPPPAAPSPQVQSCLELVARVLQRL--C
 |||||
 Db 61 LRSDDDIHVKLLHRCFV-VLHEQTPPLDPSFTSWMSQREIVERIIEIMQSGC
 |||||
 QY 96 VLAQFALLDGGARGGPEAFTTSVRSYLENTVTDALRGSGANGLLRLRYGDDVI
 |||||
 Db 118 VICARYDKYDQS-----SPILELT-SSSWEFLILKRVGHDV
 |||||
 QY 156 CALFVLVAPSCAYVCGPPYQIGRAAT-----QARPPPHASGPRRLGCERAN
 |||||
 Db 160 TSIFLPLLGKGGQVSGPPLCIKHKRTLSVHENKRRKDDNVQPTTKROWLSSAI
 |||||
 QY 210 AGVPLGLPAPG---ARRRGSSASRLPLKPRRGA-----APEPTPI
 |||||
 Db 220 DSATI-TPIVGEDVQHKREKTKTSRIYLRKRRKQKQKVFVKVDCAFCITP-
 |||||
 QY 258 HPGRTGSDRGFCVVPAPPAEATSLGALSCTRSHSPSVGRQHHAGPPST
 |||||
 Db 272 ---STNGKVSTG-----NDEMNLHIGINGSLTDFVKQAKQ-----
 |||||
 QY 318 DTPCPVVAETKHFYLS-SGDKEQLRPSFLLSSLRPSLTGARRLVETIFLGRF
 |||||
 Db 304 -----VKNKNKFKGLSETVSVIPPNHILKTLRPNCSDSKLLMNHIFGVN
 |||||
 QY 377 RRLPLRPQ---RYQMRPLFLLELGNHAQCPYVLLKTHCP-----LRAP
 |||||
 Db 357 HGKGNCPSSICLYHSLKSLKMLIGTKSSHLKMLLDKXCPVLLQEDALKSG
 |||||
 QY 425 VCARK-----PGSVAA-----PEEDTDPRRLVQLLRQHSPPQVYGFVRACLR
 |||||
 Db 417 --RRQADKLPHGSSSSQTKPKCPSEERKL-----YCTNDQVVSFTWICR
 |||||
 QY 477 LMGSRHNERFLRNTKFTISLGHAKLSLOELTWKMSVRDCAMLRSPGVCVF
 |||||
 Db 469 LLGTTQMRVLRKNTIANFVSRNRNEKCTVNOFLHKVPSPDPPFFARKE--LCQY
 |||||
 QY 537 REE-----ILAKFLHLMWSVYVVELLSRSPFYVTEFTFQKNRLLFFYKRSVMS
 |||||
 Db 527 QSESIRSTQOMCTKWSLFLFIYKLVHFNFYATESQGGRLNIYYKRSWE
 |||||
 QY 589 IRQHLKRVQLRELSAEVRQHRARPALLTSRLRFPKPDGLRPVNMVYVGA
 |||||
 Db 587 ISKALDGYLVDDAEBSRKK-----LSKFRFLPKANGVRMVLDD-----
 |||||
 QY 649 KBAERLTSRVKALFSLVANYERARRPGLLGASVLGDDTHRAWRTPVLRVRAQDP
 |||||
 Db 631 SRSQSL-----RDTHAVLKDIOKPEDVLGSSVDFDHDFFYRLNCPYLILHRSQSG
 |||||
 QY 708 FYKVDVTGAYDTIPQDRLETVIASIKPQNTYCVRYAVVQKAAHGH-----V
 |||||
 Db 687 FVAJDFKAFSDVQGLLHVQSLKDS--YILNRCFLVCCGKSNVWNLIV
 |||||
 QY 762 HVSTLTDLPYMRQVHAHQTSPLRDVIEQSSSLNEASSGLPDLVLRPMCH
 |||||
 Db 745 NPSRETSTVPYNA-----LQ-----SIVVDKGNHVRKDKDLMMVMTGNMLKN
 |||||
 QY 822 GKSYYQCCGIGPQGSILSTLCLSCYGDMMENKLPAGI-----RRDG
 |||||
 Db 793 KSFYVQIAGIQGHRLSLLCCFYFGHLERTLIYPFLEEAKDVSSKECSREEE
 |||||
 QY 863 --LRLVDVDFLLVTPHLTHAKTFLRLVGRVPGVCVVMNRKTVVNFVEDE--
 |||||
 Db 853 YKLLRFIDYLVFVTSRQDASSFYHRLKHGFKDYNCFMNETKFCINFEDKEHR
 |||||
 QY 913 --ALGGTAFVQMPAHGLFPWCGLLDDTRTLEVOQSDYSYVARTSIRASLTFNRGE
 |||||
 Db 913 FVGNGVPFVR-----WTGLLINSRTFVQVDYTRYLSGHISSTFSVAWQN
 |||||

```

201 RIETISITQNSKARK-----EVSW-
286 EGALSGTRHS--HPSVGQRGHAGPSTSRPPRPWDTPCPCPVYAEKHF-LYSSG
      :|::||::|:
220 -NSISIRFSIFRSSYKK-----FKODLYFNLSHC
343 PSFLLSLRLPSLTG-----ARRLVEIFLGSRPMMPGTPRRL----PRLPQRVY
      :|::||::|:
257 --MWLOWIFPRQFGLINAFQVKQLHKVIPLVSOQTV--VPKRLLKVYFLIEQTAA
      :|::||::|:
393 FLEILGNHAQQPYGVLLTHCHCPCLRAAVTPAAGVCAREKPGQSVAAPREEDTDPRI
      :|::||::|:
313 SLSKYNH-YCPY-IDTH-----DDE
453 ROHSPWOVQYGFVRACLRRLRYPVLGLWSRHNRERFLNRTKKFISLGKHAKLSLQJ
      :|::||::|:
335 SYSXLPNQVFAFLRSILVRVPKLINGQRIFEILKDLETFLKLSRYESFSLH
513 SVRDCAML--RRSPGCVPAEAHRILREEILAKFHLWMSVVVELLRFFFYV
      :|::||::|:
395 KISEIEMVLWGRSNAMCL--SDFEXRKQIFAIFYMLYSFIPTILOSFYYV
      :|::||::|:
570 KNRLFYFKSVMSKLOSIGIRHQLKRVQLSELSAEVRQHREARPALTLTSRLAF
      :|::||::|:
453 RNRVTYFRKDW-KLLCEPFITSXMAEAFKINENNVMDTO-KTILPPAVIRLI
630 LRPIVMYDVVGARTFREKRAELTGRVKALPSVLNYERARP-----GLLGI
      :|::||::|:
511 FRLLTNL-----RKRFLIKOMGSNKMWLST--NOTLRPVASILKHLINI
684 D---DIHEAWTF--VLVRQAQPPPELYFVKVDVTGAYDTIPODLRLTEVIAS
      :|::||::|:
559 PFNULEVYMKLUFTFKDILLKRMFG--RKXYFVRIDIKSCYDRIKQDLMFRIVKXI
738 TYCVRYAVVOKAAGHVRFKFSHTLTLDQPYMROFVAHQETSPLRDAVVJ
      :|::||::|:
617 -FVIRKYATIH-ATSDRATKNFVSEARSYEDMPFEKVQLLSMKYTS---DTLFY
798 LNEASSGLFVFLRPMCHHAVIRKGKSIVOOGIPQGSILTSLCSLCYGDMEHI
      :|::||::|:
672 WTKSSSEIFKMLEHLSGHIVKIGNSQYLKVGITPQGSILLSFCLCHFYMEDLDIE
858 RRDG-LLLRLVDDELTYTPHLTHAKTFLRTLVRGVPYEGCVNLRTVNVPFVEL
      :|::||::||::|:
732 KKXGSVLLURVDDFLFITVANKOAKFNLULSRGFEKHNFSTLEKTVINFENS
917 TAFVQMPAHGLFPWCGLLLDTRLTEV-----QSDYSSYARTSIRASULTNRRGFKQ
792 TFFNESKKR-MPPFGFSVNMRSJDLTLACPKIDEALFNSTSVELTKHMCKSF--
972 RKLFGVRLKCHS---LFLDLQVNSIQTVCTNIYKI-----LLLQAY 1010
843 --FYKILLRESSLASPAQVFIDIITNSKFNSCCNTYRLGYSWMCMQRAY 887

```

RESULT 4
T31107
telomerase reverse transcriptase - Oxytricha trifallax
C.Species: Oxytricha trifallax
C.Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Se
C.Accession: T31107
R.Bryan, T.M.; Sperger, J.M.; Chapman, K.B.; Cech, T.R.
Proc. Natl. Acad. Sci. U.S.A. 95, 8479-8484, 1998
A.Title: Telomerase reverse transcriptase genes in Tetrahymena thermo
A.Reference number: Z20985; MUID:98337940; PMID:9671703
A.Accession: T31107
A.Status: preliminary; translated from GB/EMBL/DDAJ
A.Molecule type: DNA
A.Residues: 1-1132 <BRY>
A.Cross-references: EMBL:AF060230; NID:G3342795; PID:G3342796; PIDN:A
C.Genetics:
A.Gene: TERT

GC5
otidyltransferase
6.18; Score 363; DB 2; Length 1117;
larity 20.2%; Pred.No. 9.3e-17;
Conservative 160; Mismatches 368; Indels 234; Gaps 35;

human herpesvirus 4 (strain B95-8)
herpesvirus 4, Epstein-Barr virus
985 #sequence_revision 25-Feb-1985 #text_change 23-Aug-1997
742

Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
1, 21-45, 1983
e analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus
er: A93065; MUID:85035713; PMID:6092825
742

DNA
C <BAN>
ier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H
211, 1984
uence and expression of the B95-8 Epstein-Barr virus genome.
er: A03794; MUID:84270667; PMID:6087149
tation; protein coding region
quence contains four perfect repeats (residues 149-273, 274-398, 399-52
uman herpesvirus 4 BHLF1 protein

2.9%; Score 172.5; DB 1; Length 660;
ilarity 26.1%; Pred. No.0.00064;
Conservative 16; Mismatches 159; Indels 91; Gaps 16;

QVC--GPLYVLGAATQA--RPPHASGPRRLGCERAMNHSVREAGVPLGLPAGAR 222
: : : : : : : : : : : : : : : :
RCPCAGPTTRGGAAQTHRRPPCCPSARNPGCPTWR---RRSGAQRGHPPPGAG 300
: : : : : : : : : : : : : : : :
ZGSASKSLP-LPKRPRRGAPEP-BRTFVGQSGWAHPGTRGPSDRGFV-VSPAR-- 277
: : : : : : : : : : : : : : : :
PSGFTGGRDPAAPCAPTTAAPEGCGGAAVPSGATHPERGSGPADPPAAARLPERGE 360
: : : : : : : : : : : : : : : :
-----PAEATSLEGAL-----SGTRHSHP 297
: : : : : : : : : : : : : : : :
LPDLAAARQCPCAGPPPTRSGAAQTHRRPPGPCPSARNPGCPTWRRRSAGAQRGHP 420
: : : : : : : : : : : : : : : :

```

Qy 298 SVGRQHAGGPPSTSRPRPW---DTQCP-----VYAETKHFLYSGSGDKG-
Db 421 PPGAGORPGSGPTGGRPAAPCAQTAAAPGPGGAAVPSGATPHPERGSGPADPI
Qy 343 PSFLLSSRLPSLTNGARRLVETIFLGRSPWMPG-----TPRRLPRLPQ-----
Db 481 PERQEPRLPQDLAAAGRCP----AGPPTRSGAAAOQTHRRPPGCPGSRARNKG
Qy 390 RPLFLELLGNHAAQCPYGVLLKTHCPIL--RAAVTPAAGVCAREKPGSGSVAAPPEI
Db 537 RS-----GAQRGHPPGAGORPSGPTGGRPAAPGAPGTPAAPGPGGGAAPVPSGI

RESULT 9
A59295
unconventional myosin-15 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 08-5
C:Accession: A59295
R:Liang, Y.; Wang, A.; Belyantseva, I.A.; Anderson, D.W.; Probst, F.;
an, T.B.; Fridell, R.A.
Genomics 61, 243-258, 1999
A:Title: Characterization of the human and mouse unconventional myos
A:Reference number: A59266; MUID:20021762; PMID:10552926
A:Accession: A59295
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-3511 <LIA>
A:Cross-references: GB:AF144095; NID:G6224684; PIDN:AAF05904.1; PID:
C:Genetics:
A:Gene: MGI:Myo15
A:Cross-references: MGI:1261811
A:Map position: 11:33.9
C:Superfamily: myosin motor domain homology
F:1209-1871/Domain: myosin motor domain homology <MMO>

Query Match 2.4%; Score 144; DB 2; Length 3511;
Best Local Similarity 17.6%; Pred. No. 0.59;
Matches 189; Conservative 117; Mismatches 385; Indels 380;

Qy 3 RAPRCRAVRSILRSHYREVLPLATFVRRLGPGQHWRLVORGDPAAFRALVAQCLV
Db 677 RPRLASPVGSLRQH-----PPPW-----AAPAHV-----
Qy 60 ---WDARPPFAA-----PSFRVQSLKELVARVLQRLCERGAKNV
Db 708 NWMGFAEPGTSPEVADLLAPFVPRPSFR-----ASRSRSRR-----
Qy 103 LLDGARGGPPAFTTSVRSYILPNTVTD--ALRGSGAMGLLLRRVGDVVLVHLLA
Db 752 -----SPSLIGSRRRPHLPSPQPSLSRLSPGQG-----
Qy 161 LVAPSCAYQVCPPPLYQLGAATQARPPPHASGPRRLCERANWHSVREAGVPL
Db 779 -----YHSPLGLPSLQSLSRGPFQPPPPPPRPPQSLREAP--SRRASGRLL
Qy 216 -----LPAGARRGGSGASLSLPLKX-----PRRGAAPPERT-----
Db 831 VLIGSPRPSPPPLLKHGPHRSLNLPRLPTMRRLSEPPTPAVKPWVHRAYFP
Qy 256 WAHPQRTGSDRGFCVVSPPARPAEBATSLGALSCTGTHSHSPSVGRQHHAGPS
Db 891 W---GASTGLE-----QQNQREADESTPTWTVPPLAPSVDVMDPP
Qy 316 PMDTPC-----PPVYAETKHFLYSS-----GDKEQLRI
Db 936 PMPEGIGSLRGFSRPPVPENPLEHTSPSCPEQSDRVSNLTGIFLGQHHDPG
Qy 349 SLRSLTICARLVETIFLGRSPWMPGTPRRL--PRLPORYWQMRPLFLELGNH--
Db 996 SADPSL-----EKPEEVTIGD--POPPASPEALNPTTPNKIVVSVSRKVLRLSASYP

```

2.4%; Score 142.5; DB 2; Length 1560;
 larity 29.5%; Pred.No.0.25;
 Conservative 15; Mismatches 89; Indels 51; Gaps 12:

 .YOLGAATQAPPPHASCPRRRLLGCERAWNHSVREAGVP-----LGLPAPGARRRGG 226
 ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
 .POLGSI-----PPPPASAP---PVGPHR---HFHAHGVPVQPQHYTLGRGRAPRRGAG 1415
 ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
 .RSLPLPKRP--RRGAAPPERTPVQGSGWAHPGRTGRFSDRGFCVSPARPAEANTSL 285
 ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
 .QAFPHGRHPLHQTPSLPLYSAPQPPAH---KQGPKEIFISHHPQMMPAAGAAGG 1472
 ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
 L-STRHSHPSVGQRHHAGPPSTSR---PPRPWDTCPVPVYAETKFH----- 331

Query Match	2.4%;	Score 140.5;	DB 2;	Length 1892;
Best Local Similarity	23.4%;	Pred. No. 0.44;		
Matches 111;	Conservative	47;	Mismatches 195;	Indels 121;
QY	44	PAAFRALVAQCLVCPWMDARPPAAPSPQVSCLEKELVARVLQRLCERGAKNVL		
Db	366	PSLHLPQQQPVILVP---QRPAPPQERLPRLYSSTTRPAGGSPRGCAVQNNI		
QY	104	LDGAGGGPEAPTTSVRS-----YLNTVTTALRGSGAWGLLLRRVGDDVLVHH		
Db	423	EDTSSGAGEVTSRSRSRTQVRRPAPVTPASDIPTGS-PYGAM-----		
QY	159	FVLVAPSCAYOVCGPPLYOLGAATCARPPPHASG-----PRRLGCG-----		
Db	466	YAVVMFQ--RSLPAPPKTKGASNASAGLPPPSAPAEAAQQOHNRCPPSSSRPS		
QY	205	HVRVAGVPLGLPADGAR-----RRGSGASRSLP-----LPKRP--RGAA		
Db	524	HAAREQ--PLQPQPPQKRALPQRHQFORAETAKSQLPPMRLEADPFYSBELI		
QY	250	PVYGQSWAHPGKTRGPSDR-GFCVVSPARPA-----BEATSELEGALSTRHSP		
Db	581	---EGADGNASTQSGHRGGHVSIVPSQQQLSLSHEDIJLSAMLASATVAAP		
QY	303	HHAGPSTSRPRPMDTPCPPVYATKFLYSGDGKQLRPSFLLSLSRPSLTG		
Db	638	PYAGTAPDGPRLHVMPPPIIQRP---YAATEEE-----G		
QY	362	ETIFLGSPWMEGTPRRLPRLPQRYWQMRPLFELLGNHAQCPYG--VLLKTHC		
Db	679	RKVTAQESDAPFRHSP-----FAETHLLHSRGAADGAGEAAAKETREI		
QY	419	---VTPAAGVCAREKQO-----GSVAAPPEEDTDPRELQV---LLRQHSSP		
Db	729	EAVTAMTTAGVQSSKKPQOLQHPDGSG---PNGDDVD--ELLEADDLLIMOPSRP		

```

RESULT 12
EDBE1F
Immediate-early protein IE180 - suid herpesvirus 1 (strain Indiana-F1
C.Species: suid herpesvirus 1
C.Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 16-F8
C.Accession: S04713
R:Cheung, A. K.
Nucleic Acids Res. 17, 4637-4646, 1989
A.Title: DNA nucleotide sequence analysis of the immediate-early gene
A.Reference number: S04713; NUID:89315207; PMID:2546124
A.Accession: S04713

```

DNA
60 <CHE>
herpesvirus immediate-early protein IE175
binding; early protein; transcription regulation
2.3%; Score 140; DB 1; Length 1450;
Conservative 35; Mismatches 163; Indels 158; Gaps 27;
ilarity 24.3%; Pred. No. 0.33;
RALVAQCLVCPWMDARPPAAPSPQVSKLXELVAVLQRLCERGAKNVLAFFGALLD 105
RGVLERLLPC-PLRLPAPAPALGPACLEEVTAALL-ALRD 746
RG-GPPE-----AFTTSVRSYLPNTVTDALRGSGAMGLLRRVGGDVLVHLLAR 155
PGAGPARRQQAADSVLAVRTVPLVRYSDGARAREAAW-----TYA 791
LEVLVAPSCAVQVGPPLVQYQGAOTARPAPHASGPRRLGCEAANH-----S 206
LF---AFA---NVAGAL-----AFAARPGABAP-----GLPLMPEQGLVVPAPA 837
EAGVPLGLPAPG-----ARRGGASRSPLPKPRRGAAPPEPTPVQGSWAHPGRT 262
AAGAPSLPGSGSPSPASTKSGSTKSSGTSKLSGSS-----GYARLPRRR 887
PSDRGFCVSP-----ARP--ABEATSLEG-ALSGTRHSHPSVGRQHAGPPSTSRP-- 313
PSAFAAQEAPRACARRPGDGEDEGLSGALRGDGHGRD--DEEDRGPRRKRSLG 945
PRPMDTCPVVAETHKFLYSSGDKQLRPSFLLSRLPSLTGARRLVETIFLGSRPW 371
PAP--DPAPALVSSSS--SSSEDDRLR-----RP-----LGPMPPE 980
GTPRLRLPQRYWQMRPLFLELGNHAQCPYGVLLKTHCP-----L 415
APDGGFRVPAG-----ETHTPRPSAALAAAYCPPEVARALVDQEVPELM 1028
AVT--PA--AGVCAREKPGQSVAAPEEDTDPRLVQLLRQHSSPWQV 461
ALTFDPAALAHIAIA--RGAAGAP-----LRRRAAMRQIADPEDV 1069
ATP-binding protein - Deinococcus radiodurans (strain R1)
coccus radiodurans
999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
311
en, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
Vanathavan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
Venter, J.C.; Fraser, C.M.
1-1577, 1999
sequence of the radioresistant bacterium Deinococcus radiodurans R1.
er: A75250; MUID:20036896; PMID:10567266
inary
DNA
2 <WHI>
es: GB:AE002048; GB:AE00513; NID:G6459929; PIDN:AAF11688.1; PID:G645993
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1
2.3%; Score 139.5; DB 2; Length 552;
ilarity 22.3%; Pred. No. 0.094;
Conservative 38; Mismatches 196; Indels 233; Gaps 27;
SGAWGLLRVGGDVLVHLLARCAFLVAP-----SCAYQVCGP 173
S---RLQFRVSGKSTRIRFTSTESLFCLLAPLGLTIASSGTGSIHSSDVAAATTAARP 80
---LYQLGATQARPPPHASGPRRLG-----C 199

Db 81 PCTRHRRGAG--AAPRFADGPARRGAAAGARRRRQNHAARRASCARE
QY 200 ERAWNHSVREAGVPLGLPAPGARRGGASRSPLPKPRRGAAPERTPVGC
Db 139 AERTGSAPFRAGA--AYPERGGARRGVLSHSLKLTDRARRAAGRGGRTPAAV
QY 260 GTRCPSPDRGFCVSPAPAEATSEALSGTRHSHPSVGRQHAGPPSTSR
Db 195 -RTTPVGRG-----DYTRRGALAGARLSHPLA-----RAAPPDAGE
QY 320 PCPPVVAETHKFLYSSGDKQLRPSFLLSRLPSLTGARRLVETIFLGSRPWME
Db 233 -----RPDAAA-----E
QY 380 PRLPQRYWQMRPLFLEL---LGNH-----AOCYPGVLLKTHCPRL
Db 247 HRWPSRSPRRRRRAAPFGPCGGHGVGAGDPPARGSPDAELAHGVRSGRTERR
QY 423 -----AGVCAREKPGQSVAAPEEDTD-----PRLVQLLRQHSSPWQV
Db 307 RSPRSGGASTGPLCGTAAVELTDAEVRNCHRGALGPLSWTAAAGH---WLV
QY 465 VRACLRRLVP-----PGLWGSRHNRERFLNTKFKFISLGHAKLSLQELTWKMSV
Db 364 GKSTLARLIAGELHDPALGGS--VARPFL-----A
QY 520 LRSPSGVGCVAAPAEHLREELAKELHWMVSVVVELLSRFPYVTE-----TTF
Db 397 RRRITG---LVSAAVGIRQSGVSGREWLG---DVIAAFAGTEGFTGDVTA
QY 575 FYRKSVMKSLQSIGIR-----OHLKRVQLRELSEAEVRQHRBARPALL
Db 446 -----WDAVGTAEELGELSDVQALSGQLRLLLAARAAVHR-PRLLLL
QY 624 I 624
Db 499 V 499
RESULT 14
S27923
Gene LF3 protein - human herpesvirus 4
C:Species: human herpesvirus 4, Epstein-Barr virus
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-J
C:Accession: S27923
R.Parker, B.D.; Bankier, A.; Satchwell, S.; Barrell, B.; Farrell, P.
submitted to the EMBL Data Library, August 1990
A:Description: Sequence and transcription of Raji Epstein-Barr virus
A:Reference number: S27923
A:Accession: S27923
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-924 <PAR>
A:Cross-references: EMBL:M35547; NID:G330420; PIDN:AAA45896.1; PID:G
C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxy
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Best Local Similarity 27.0%; Pred. No. 0.23; Indels 55;
Matches 80; Conservative 25; Mismatches 136;
QY 179 GAATQARP-----PPHASGPRRLGRCERAWNHSVREAGV-----PLGLPAPGAR
Db 26 GAADPADPVGHAPAPRAPGPEPRTRLOPA---TPRRSGAADPADPVGHGA--AP
QY 229 SRSLPLPKPRRGAAPERTPVQGSWAHPGRTGSDRGFCVSPAPAEAE
Db 81 PTRLOPATPRRSGAADP-ADPVG-----HPAAPRAGPPEPRTRLOPATPRRS
QY 289 LSGTGHSHPSVGRQHAGP-----PSTSR-----PPRPMDTCPVVAETHKFI
Db 135 PVG-----HPAAPRAGPPEPRTRLOPATPRRSGAADPADPVGHGAAP-----

JLRPSPILLSRLPSLTGARLVVETIFLGRSPPWPG-TPR-RL-PKLPORYQMPLFL 394
: : : : :
RTR-----LQATPRSAGADPADPVGHPAAPRAPGPEPTRILQATPRSGAADP--A 235
:
GNHAOCPYGVLLKTHCPLEAAVTTPAAGVCAREKPGSQSVAAPEBEDTDPRLVQ 450
: : : : :
HG-HPAAPRAPGPEPTRILQATPRSGAADPADPVGHPAAPRAPGPEPTRILQ 290
:

ate receptor chain NMDAR2D-1 - rat
; norvegicus (Norway rat)
#sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
119
yoshi, K.; Sugihara, H.; Sakurada, K.; Kadotani, H.; Yokoi, M.; Akazawa
8, 2836-2843, 1993
ur characterization of the family of the N-methyl-D-aspartate receptor s
r: A45219; MUID:93155102; PMID:8428958
119
nary; not compared with conceptual translation
mRNA
5' <ISH>
source: brain
extracted from NCBI backbone (NCBIP:124264)
methyl-D-aspartate receptor 2D; glutamate receptor homology
glutamate receptor homology <GRH>

2.3%; Score 135; DB 1; Length 1356;
ilarity 27.2%; Pred.No.0.67;
Conservative 16; Mismatches 102; Indels 118; Gaps 22;

ARPFPAA-----PSFRQVSCLKELVARVLQLCERGAKNVLAFGFALLDG----- 106
AAPFPYALDEPS-----PSSSEDSLSGLASLGSLGLEPWFA 1124
----ARGGPPEAFTTSVSYLPNTVTVDALRG--SGAWGLLLRRVGDDVLVHLARCA 157
YPVAERLGGPPGYWSV-----DKLGGWRAGWDYLPPRCGP---AWHCRA 1172
TVAP-----SCAYQC-----GPLYQLGAATQARPPPHASGP-----RRLCGERAWN 204
LLPPRHLSCHDLGGGWAPP-----PPFWAAGPPPRRARCGCPRPHP 1221
REA-GVPLGLHPAPCARRR--GG-----SASHSL-PLPKRPRRGAAPEPT-PVG 252
RASRAFAAAPHHHRARRAGGDWFFPPPATSRSLDELRSR-----CP-FHTGTDTG 1276
WAHPCRTGPSDRGCFCVVSP-----ARPAEBATSLEGALSCTRHSFHSVGRQHA 305
WAHAGALR-----ISPAMSPRYDAAPAPTTPAAPSVSA---GHGPRGRAKT 1324
STR-----PR--PWDTFCCP 323
WVKDRNGPQRTPPGAASCAP 1348

April 22, 2004, 00:17:19
s

GenCore version 5.1.6
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tein search, using sw model

April 21, 2004, 21:01:06 ; Search time 22 Seconds
(without alignments)
2679.246 Million cell updates/sec

JS-09-424-686f-2
1961

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ILOSUM62

lapop 10.0 , Gapext 0.5

41681 seqs, 52070155 residues

its satisfying chosen parameters: 141681

length: 0

length: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

SwissProt_42:*

s the number of results predicted by chance to have a
er than or equal to the score of the result being printed,
ved by analysis of the total score distribution.

SUMMARIES

Entry	Accession	Length	DB	ID	Description
00.0	1132	1	TERT_HUMAN	O14746	homo sapien
58.8	1122	1	TERT_MOUSE	O70372	mus musculus
10.0	988	1	TERT_SCHPO	O13339	schizosacch
7.5	1031	1	TERT_EUPAE	O00939	euplotes ae
6.6	1132	1	TERT_OXYTR	O76332	oxytricha t
6.1	1117	1	TERT_TETH	O77448	tetrahymena
6.0	884	1	TERT_YEAST	O06163	saccharomyc
3.0	3530	1	MY15_HUMAN	Q9ukn7	homo sapien
2.9	660	1	YHL1_EBV	P03181	epstein-bar
2.5	653	1	SF01_MOUSE	Q64213	mus musculus
2.5	1003	1	MBD6_HUMAN	Q96dn6	homo sapien
2.4	3511	1	MY15_MOUSE	O9qz24	mus musculus
2.4	1461	1	IE18_PRVIF	P11675	pseudorabie
2.3	997	1	IF2_BORPE	Q7vy22	borderella
2.2	623	1	DTX1_XENLA	Q8aw93	xenopus lae
2.2	946	1	IP3L_HUMAN	P27987	homo sapien
2.2	1185	1	DRPL_HUMAN	P54259	homo sapien
2.2	657	1	DEND_HUMAN	Q94850	homo sapien
2.2	888	1	SM6B_HUMAN	Q9h3t3	homo sapien
2.2	1446	1	IE18_PRVKA	P33479	pseudorabie
2.2	621	1	V540_HSVBC	P54817	bovine herp
2.2	2716	1	OSA_DROME	Q8in94	drosophila
2.2	709	1	ANDR_RABIT	P49699	oryctolagus
2.2	628	1	V70K_TYV	P10357	turnip yell
2.1	1048	1	SRA4_RAT	Q83627	rattus norv
2.1	1226	1	CDN1_HUMAN	Q81wy9	homo sapien
2.1	505	1	WASL_BOVIN	Q95107	bos taurus
2.1	997	1	IF2_BORBR	Q7whg2	borderella
2.1	720	1	GTSE_HUMAN	Q9ny23	homo sapien
2.1	1298	1	ICP4_HSV1	P08392	herpes simp
2.1	503	1	WAIP_HUMAN	O43516	homo sapien
2.1	653	1	DEND_RAT	P50617	rattus norv
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34	123	2.1	646	1	VP40_HSVB	P28936	eq
35	123	2.1	916	1	RTJK_DROME	P21328	dn
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42	121.5	2.0	234	1	PRPM_HUMAN	P10161	hoi
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44	121.5	2.0	942	1	M3K2_MOUSE	Q9wtl6	mu
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ALIGNMENTS

RESULT 1
TERT_HUMAN
ID TERT_HUMAN STANDARD; PRT; 1132 AA.
AC O14746; O14783;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit) (HEST2).
DE TERT OR TERT OR EST2 OR TCS1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=97400623; PubMed=9252327;
RA Nakamura T.M., Morin G.B., Chapman K.B., Weinrich S.L., Andrews Lingner J., Harley C.B., Cech T.R.;
RT "Telomerase catalytic subunit homologs from fission yeast and h Science 277:955-959(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97433088; PubMed=9288757;
RA Meyerson M., Counter C.M., Eaton E.N., Ellisen L.W., Steiner P., Caddle S.D., Ziaugra L., Beijersbergen R.L., Davidoff M.J., Liu Bacchetti S., Haber D.A., Weinberg R.A.;
RT "HEST2, the putative human telomerase catalytic subunit gene, is regulated in tumor cells and during immortalization.";
RL Cell 90:785-795(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99267414; PubMed=10333526;
RA Wick M., Zubov D., Hagen G.;
RT "Genomic organization and promoter characterization of the gene encoding the human telomerase reverse transcriptase (hTERT).";
RL Gene 232:97-106(1999).
RN [4]
RP SEQUENCE FROM N.A.
RA Londono-Vallejo J.A.;
RT "Sequence of a BAC carrying the entire hTERT gene.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential for the replication of chromosome termini in most eukaryotes. It elongates telomeres. It is a reverse transcriptase that adds simple sequence repeats to chromosome ends by copying a template sequence within the RNA component of the enzyme.
CC -I- SUBUNIT: Interacts with PINX1.
CC -I- SUBCELLULAR LOCATION: Nuclear.
CC -I- DISEASE: Activation of telomerase has been implicated in cell immortalization and cancer cell pathogenesis.
CC -I- SIMILARITY: Belongs to the reverse transcriptase family. Telomerase subfamily.

CC This SWISS-PROT entry is copyright. It is produced through a col

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email to license@isb-sib.ch).

50; AAC51672.1; -
167; AAC51724.1; -
394; AAD30037.1; -
393; AAD30037.1; JOINED.
385; AAG23289.1; -
T03844.
11730; TERT.
-;

596; C:telomere; TAS.
121; E:telomeric template RNA reverse transcriptase. .; TAS.
R000477; KVTse.
R003545; Telomerase_RT.
78; rvt; 1.
1365; TELOMERASERT.
RNA-directed DNA polymerase; Telomere; Nuclear protein;

516 516 D -> G (IN REF. 2).
132 AA; 126996 MW; 94E35469CA33A0 CRC64;

100.0%; Score 5961; DB 1; Length 1132;
100.0%; Pred. No. 0;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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IFLGSRPMPGCTPRLPLPORYQWMLPFLLELGNHAQCPYGVLLKTHCPRAAVT 420
IFLGSRPMPGCTPRLPLPORYQWMLPFLLELGNHAQCPYGVLLKTHCPRAAVT 420

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GVCCAREKPGSVAAPPEEDTPRLVQLRQHSPPQVYGFVRACTRLVPPGLWGS 480

IFRRFLNNTKFTISLGGKAKLSLQELTWQSVYRDCAWLRRSPGVGCVPAAEHLREEI 540
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661 LFSVLNVERARRPPGLGASVLGLDDIHRAWRTFVLVRVAQDPPPELYYFKVDVT
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721 PQDLRLTEVIASIIKPNQTYCVRVAVVQKAAHGHVRKAFKSHVSTLTLQVPMR
721 PQDLRLTEVIASIIKPNQTYCVRVAVVQKAAHGHVRKAFKSHVSTLTLQVPMR
781 QETSPLRDADVIEQSSSINEASSGLFDVFLRFMCHHAVIRIGKSYVQCGIPQG
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841 LCSLCYGMENKLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRLTVRGVPEY
841 LCSLCYGMENKLFAGIRRDGLLRLVDDFLVTPHLLTHAKTFLRLTVRGVPEY
901 RKTVVNFVDEALGGTAFVQMPAHGLFPWCGILLDTRTLLEVQSDYSYARTSI
901 RKTVVNFVDEALGGTAFVQMPAHGLFPWCGILLDTRTLLEVQSDYSYARTSI
961 NRGFKAGNNMRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFAH
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RESULT 2

TERT MOUSE
ID TERT MOUSE STANDARD; PRT; 1122 AA.
AC 070372; 035432;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, last sequence update)
DT 28-FEB-2003 (Rel. 41, last annotation update)
DE Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase cataly
DE subunit).
GN TERT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98241176; PubMed=9582020;
RA Greenberg R.A., Allsopp R.C., Chin L., Morin G.B., DePinho R.A.;
RT "Expression of mouse telomerase reverse transcriptase during
RT development, differentiation and proliferation.";
RL Oncogene 16:1723-1730(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98393658; PubMed=9724727;
RA Martin-Rivera L., Herrera E., Albar J.P., Blasco M.A.;
RT "Expression of mouse telomerase catalytic subunit in embryos and
RT adult tissues.";
RN [3]
RP Proc. Natl. Acad. Sci. U.S.A. 95:10471-10476(1998).
RP SEQUENCE OF 550-616 FROM N.A.
RA Drissi R., Cleveland J.L.;
RT "Partial sequence of Mus musculus telomerase catalytic subunit
RT homolog.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Telomerase is a ribonucleoprotein enzyme essential
CC the replication of chromosome termini in most eukaryotes. It
CC elongates telomeres. It is a reverse transcriptase that adds
CC simple sequence repeats to chromosome ends by copying a temp
CC sequence within the RNA component of the enzyme.

Interacts with PINK1 (By similarity).
 TLR LOCATION: Nuclear.
 TY: Belongs to the reverse transcriptase family.
 se subfamily.

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 : -profit institutions as long as its content is in no way
 : this statement is not removed. Usage by and for commercial
 : quires a license agreement (See <http://www.isb-sib.ch/announce/>
 : mail to license@isb-sib.ch).

11; AAC09323.1; -;
 11; AAC34821.1; -;
 35; AAB84200.1; -;
 2709; Tert
 R000477; RTase.
 R003545; Telomerase RT.
 8; rvt; 1.
 365; TELOMERASERT.
 RNA-directed DNA polymerase; Telomere; Nuclear protein;

553 553 I -> V (IN REF. 3).
 122 AA; 127977 MW; F85266905DD6558C CRC64;
 larity 58.8%; Score 3505; DB 1; Length 1122;
 Conservative 122; Mismatches 260; Indels 52; Gaps 13;

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 PKRPRGAAPPEPTFVQGSWAHPGTRGRGSDRGFCVVSFAR-----PAREATSL 286
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 SDSLIS-GSVCKKHKPSSTLSLSPRQNAFQLRP-FIETHFLSRGDDGGERLNPSF 350

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 NLOPLNLTGARLVETTFILGSRPMWGPTRRLPLRPQYQWRPLFLELLGNHAQCPY 410

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 LRSHCRFTANQQVTDAL-----NTSPHLLMDLLRLHSSPPQVY 452

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 KDRVPAAEHLRLREILAKFLHLMVSVYVELLSFFVYTTTFQKNRLLFFYKSVMS 572

SIGRHLKRVQLRELSAEVRQREARPAALLTSRLRFLPKDGLRPIVMDYVGA 642
 SIGVRHLRLVRLRELSQEEVRHHQDTWLAMPICRLRFLPKDGLRPIVNMYSMTG 632

QY 643 RTPREKRAEELTSRVKALSVLVNRYARRPGLLGASVLGDDIHRATVFLR
 Db 633 RALGRKQAOHQFTORLKTFLSMLNRYETKPHLSSVGLGNDIYRTWRAFLR
 QY 703 PPELYFVKVDVTGAYDTPIDORLTEVIAI-K-PONTYCVRYAVVOKAAHGHV
 Db 693 TPRMYFVKADVGTGAYDAIPQGLVEVVANMRHSESTYCIROYAVVRDSQGV
 QY 762 HVSTLTDLQPMRFVHAHQET--SPLRDAVVIQSSSLINEASSGLFDVFLRFM
 Db 753 QVTTLSDLQPMRGFLKHLQDSASALRNSVIEQSI-SMNESSSLFDFLHFL
 QY 820 IRGKSVYCCGIGPOGSLSTLLGSLCYGDMENKLFAGIRDGLLLRLVDDFLV
 Db 813 IGRCTYCCGIGPOGSSLSLLCSLCFDMENKLFAGVQDRDGLLRVDDFLV
 QY 880 AKTFLRTLVRGVPYGCVMNLRTVNVFPVVEDEALGGTAFVQMPAHGLFPWCGLI
 Db 873 AKTFLSTLVHGVPEYGCVMNLQKTIVNFPVPGTLLGGAAPQLPAHCLFPWCGLI
 QY 940 LEVQSDYSSTARTSIRASLTFRNGFKAGRNWRKLFQVLRKCHSLFLDLQVNSI
 Db 933 LEVFCDSYGYAOTSIKTSLTFQSVFKAGTWRNKLKSLVLRKCHGLFLDLQVNSI
 QY 1000 NIYKILLQAVRFHACVQLQPFHQVQWKNPTFLRVISDTSASLCYSILKAKNAG
 Db 993 NIYKIFLLQAVRFHACVQLQPFHQVQWKNPTFLRVISDTSASLCYSILKAKNAG
 QY 1060 GAAGPLFSEAVQMLCHQAFLLKLTTRHVTYVPLIGSLRTAQTLRSKLPGLTTLT
 Db 1053 GS---PPEAAHMLCYQAFLLKLAHSVYKLLGPLRTAQKLLCKRLPEATMT
 QY 1120 NPALPSDFKTILD 1132
 Db 1110 DPALSTDFQTILD 1122

RESULT 3

TERT_SCHPO
 ID TERT_SCHPO STANDARD; PRT; 988 AA.
 AC OI3339; OI3338;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catal;
 DE subunit).
 GN TERT1 OR SPBC29A3.14C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=97400623; PubMed=9252327;
 RA Nakamura T.M., Morin G.B., Chapman K.B., Weinrich S.L., Andrews
 RA Lingner J., Harley C.B., Cech T.R.;
 RT "Telomerase catalytic subunit homologs from fission yeast and hu
 RL Science 277:955-959 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandran M.A., Lyne M., Lyne R., Stewart
 RA Scouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson
 RA Holroyd S., Horsby T., Howarth S., Huckle E.J., Hunt S., Jagels
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.

Qy	166	CAYQVCGPPLYQLGAATQARPPPHASGPRRRIGCERAWNHSYREAGVPGLGPAPAA
Dd		: : : :
Dd	176	NYLQISGIPLFK-----NNVFETV-----
Qy	226	GSASRSLPIPKPRRCGAPEPERTVPGOGSWAHPCRTGPSDRGCVCVSPARPAA
Dd		: : : :
Dd	201	RITETSITONKSGARK-----EVSW-----
Qy	286	EGALSGTRHS--HPSVGROHHAGPSTSRPPRPMDTPCPVPVAETHKF-LYSSGI
Dd		: : : : : : : :
Dd	220	-NSISISRFSIYRSYKK-----FKQDLYPNLHSDCI
Qy	343	PSFLSSLPSLTG-----ARRLVETIFLSRPMMPGTPTRL-----PRLPQRYI
Dd		: : : : : : : :
Dd	257	--MWLQWIFFRGFLINAFQVKLHKVIPVLSQSTV--VPKRLLIKVYPLIBQTAL
Qy	393	FLELLGNHAQCYPGVLLKTHCLPRAAVTPAAGVCAREXPQSQAPEEDTDPRI
Dd		: : : : : : : :
Dd	313	SUSKVNH-YCPY---IDTH-----DDE-----
Qy	453	QHSSPVQVYGVRACLRRLVPPGLWSGRHNERRFLRNTKKFIPLGHKAHLSQLQ
Dd		: : : : : : : :
Dd	335	SYSLKDNQVFAELRSILRVFPKLWNQRNFTEILKDLETFLKLSRYESFSLH
Qy	513	SVRDCAWL---RRSPGVGCVPAAEHRLBREEILAKFLHLMVSYVVVELLSRFVY
Dd		: : : : : : : :
Dd	395	KISEIEWLVLGKRSNAKMCL--SDPEKRKQIFAEBFYWLNSYFIIPILQSFFYI
Qy	570	KNLFPYRKSVMSKLSQSIGIRHLKXVLRELSEAVRQHREARPALITSRLF
Dd		: : : : : : : :
Dd	453	RNKTVVFRKDIW-KULCRPFITSMQWEAFKINENNVMMDTQ-KTTLPPAVIRLI
Qy	630	LRIPIVMQDVVGARTFREKEAERLTNVKALFSLVNYERARRP-----GLLG/I
Dd		: : : : : : : :
Dd	511	FRLLTNL-----RKRFLIKGSKMKMLVST--NQTLRPVASILKHLLNI
Qy	684	D----DIHRAWRTF---VLRVRAQDPPELPXYFVKVDVTGAYDTIPQDRLTEVIASJ
Dd		: : : : : : : :
Dd	558	PENLEVYMKLLTFKKDLKHMFG--RKKYFVRIDIKSCYDRIKQDLMFRIVKKG
Qy	738	TYCVRYAYVQAAHGVRKAFKSHVSTLTDLQPYMRQFVAHLOETSPIRDANV
Dd		: : : : : : : :
Dd	616	-FYIRKYATIH-ATSDRATKNFVSEAFYDFMWPFVKVQLLSMKTS---DTLFY
Qy	798	LNEASSGLFDVFLRFWMCHAVRIGKSYYOCQIPOGSIILSTLCSLCYGDMEINI
Dd		: : : : : : : :
Dd	671	WTYSSEIEFMKLKEHLSGHVIGINSQVYLQKVGIPQGSILSFLCHFWMEDLIDI
Qy	858	RRDG-LLRLVLDDFLVTLPHLTHAKTFURTLVRGVEYGCVVNLRLKTVVNPFEI
Dd		: : : : : : : :
Dd	731	KKKGSVLLRVDDDFLFTVNKKDAKKFLNLIRLGFKEHFNFTSLEKTVINPENSI
Qy	917	TAFVQMPAHGLEFPWGCLLDRTTLEV-----QSDYSYVARTSIRASLTFNRGFKI
Dd		: : : : : : : :
Dd	791	TFINESKKR--MPFFGFSVMKRSRDLTACLKPIDEALFNSTSVELTKHMGKSF--
Qy	972	RXLFGVLRCLKHS---LFLDLQVNSLQVCTNVIKI-----LLAQY 1010
Dd		: : : : : : : :
Dd	842	--FYKILLRSSLASFAQVVIDITHNSKFNSSCCNIYRLGYSCMCRAQAY 886
RESULT 4		
TERT_EUPAE		
ID_TERT_EUPAE	STANDARD;	PRT; 1031 AA.
AC	O00939;	
DT	30-MAY-2000 (Rel. 39, Created)	
DT	30-MAY-2000 (Rel. 39, Last sequence update)	
DT	30-MAY-2000 (Rel. 39, Last annotation update)	
DE	Telomerase reverse transcriptase (EC 2.7.7.-) (Telomerase catalytic subunit) (Telomerase subunit P123).	
OS	Euplotes adiculus.	
OC	Eukaryota; Alveolata; Ciliophora; Spirotrichea; Hypotrichia;	
OC	Euplotidia; Euplotidae; Euplotes.	

Q E R K K F F F 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 A D I D E D E K X X B Y 25 DE 27 DE 29 DE 31 DE 33 DE 35 DE 37 DE 39 DE 41 DE 43 DE 45 DE

(Rel. 40, Last sequence update)
(Rel. 43, Last annotation update)
Unconventional myosin-15).

015.

(Human).
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Cheria; Primates; Catarrhini; Hominidae; Homo.
606;

M N.A., SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
1762; PubMed=10552926;
ng A., Belyantseva I.A., Anderson D.W., Probst F.J.,
Miller W., Touchman J.W., Jin L., Sullivan S.L.,
Camper S.A., Lloyd R.V., Kachar B., Friedman T.B.,
ation of the human and mouse unconventional myosin XV
sible for hereditary deafness DFNB3 and shaker 2",
243-258(1999).

TENCE FROM N.A., AND VARIANTS DFNB3 TYR-2111 AND PHE-2113.

ng Y., Fridell R.A., Probst F.J., Wilcox E.R.,
Morton C.C., Morell R.J., Noben-Trauth K., Camper S.A.,
of unconventional myosin MYO15 mutations with human

deafness DFNB3.",
1447-1451(1998).

Myosins are actin-based motor molecules with ATPase
gibly divergent tails are presumed to bind to membranes.
nts, which would be moved relative to actin filaments (By
ty). May play a role in the formation or maintenance of
n-rich structures of the inner ear sensory hair cells.

LAR LOCATION: Cytoplasmic.

PECIFICITY: Highly expressed in pituitary. Also expressed
levels in adult brain, kidney, liver, lung, pancreas,
y, and skeletal muscle. Not expressed in brain. In the

Defects in MYO15A are the cause of autosomal recessive
omic deafness type 3 (DFNB3) (MIM:600316).

TY: Contains 1 myosin-like globular head domain.

TY: Contains 1 FERM domain.

TY: Contains 3 IQ domains.

TY: Contains 1 MYTH4 domain.

TY: Contains 1 SH3 domain.

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mail to license@isb-sib.ch).

94; AAF05903.1; -

76; -; NOT_ANNOTATED_CDS.

AS9266.

IBR2.

7594; MYO15A.

-

05; P:hearing; TAS.

R000299; Band 4.1.

R000048; IQ region.

R001609; myosin_head.

R000857; MYTH4.

R001452; SH3.

2; IQ; 3.

3; myosin_head; 1.

4; MYTH4; 2.

193; MYOSINHEAVY.

0355; myosin_head; 1.

95; B41; 1.

DR SMART; SM00015; IQ; 3.
DR SMART; SM00242; MYSC; 1.
DR SMART; SM00139; MYTH4; 2.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00660; FERM_1; FALSE_NEG.
DR PROSITE; PS00661; FERM_2; FALSE_NEG.
DR PROSITE; PS00057; FERM_3; 1.
DR PROSITE; PS50096; IQ; 3.
DR PROSITE; PS50002; SH3; FALSE_NEG.
KW Myosin; ATP-binding; Actin-binding; Coiled coil; Repeat; SH3 dom
KW Calmodulin-binding; Disease mutation; Deafness.
FT DOMAIN 1 1887 MYOSIN HEAD-LIKE.
FT DOMAIN 1888 2029 NECK OR REGULATORY DOMAIN.
FT DOMAIN 2030 3530 TAIL.
FT DOMAIN 1323 1350 COILED COIL (POTENTIAL).
FT DOMAIN 1792 1799 ACTIN-BINDING (POTENTIAL).
FT DOMAIN 1902 1924 IQ 1.
FT DOMAIN 1925 1954 IQ 2.
FT DOMAIN 1955 1976 IQ 3.
FT DOMAIN 2867 2953 SH3.
FT DOMAIN 3209 3530 FERM.
FT NP BIND 1315 1322 ATP (POTENTIAL).
FT VARIANT 2111 2111 N -> Y (in DFNB3; family from Bengk
FT VARIANT 2113 2113 I -> F (in DFNB3; Indian family).
FT /FTID=VAR_010303.
FT /FTID=VAR_010304.
SQ SEQUENCE 3530 AA; 395171 MW; 3D103923D4BCBE4A CRC64;
Query Match 3.0%; Score 176.5; DB 1; Length 3530;
Best Local Similarity 20.6%; Pred. No. 0.0068;
Matches 263; Conservative 144; Mismatches 392; Indels 475;
QY 107 ARGGPPEAFETS-----VRSYLP-----NTVTDALRG
Db 2313 SRGPKVFGNSWDSDEDMSTRPQHEMKVLDSDGYSHNDGNGTETEAQRG
QY 139 LLRLRRVDDVLHLLARCALFVLAVP-----SCAYQVCGPPLYQLGA
Db 2372 QESDLSGEPAVPHKGLDCLVLSLFDVLSYGDADLEKPTALAYRMKGQGPQGGG
QY 182 -TQARPP-----PHASGPRRLGGERAWHNSVREAGV---PLGLPAPGARRRGGAS
Db 2432 DTPRREPPEKPIPLGLDASTLALQAFIH--KQAVLLARGMTLQATLQOQPLSAA
QY 234 LPKRRRGAAPPERTPVGGGWAHGRTRGSDRGFCVVSPARPAEETSLEGA
Db 2490 AEKPP-----APEAQTSTVGTGPPAKVLR-----ATPKPLAPA-----
QY 294 HSHPSVGRQHHAGPPPTSPRPMDTPCPVYA-----ETKHFVSSGDKBQLR
Db 2525 -----PLAKAPRLPIKPAAPVLAQOQASPET-----TSPSELVR
QY 348 SSLRPSLTGARLVEITFLGSRPMPGTERRLPRLPQRYWQRP-----LFLE
Db 2566 SEHFQPT--QOLKNIVRYQQPFRGRPEALRKDGKGVFMKRPDPHEALMLK
QY 401 ACPYG-----VLLK--THCPLRAAVTPAAGVCAREKPGQSVAAPEE-EDTD
Db 2624 LAAPCTQVSREAVALKPVTAP-RPSNAPTSAL-----PSSLEPPPELTQTR
QY 450 ---QLRQHSSPMQVYGFVR-----ACLR--
Db 2678 NPNFYGYQDAPWKI--FLRKEVFPKDSYHPVQLDLLFRQLHDTLSEACLRIS
QY 473 VPPGLWGRSHNERRFLNRTKKEISLG-KHAKLSLOELTWKMSVRDCAWLRSPGV
Db 2736 RMKALFAQNG-----LDQKPLVTESVKRAVVSTARDTWEV-----YFSRIFPAT
QY 532 ASHRLREETLAKFLHLMVSVVYVLLR-----SFFVYVTTTF
Db 2786 G-----VQLLA-----VSHVGIKLLRMVKGQEGAGGLVLRYSFADILFTVM
QY 573 LFFYRKSVMSKLSQSIGIROHLKRVOLRELSEAEVQRHREARPAALLTSRLRFPKPK.

STANDARD; PRT; 660 AA.

(Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 36, Last annotation update)
BHLF1 protein.
virus (strain B95-8) (Human herpesvirus 8; HHV-8; Kaposi's sarcoma-associated herpesvirus; KSHV; Lymphocryptovirus. 3377;

M. N.A.
 0667; PubMed=6087149;
 Kier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
 Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
 , Barrell B.G.
 and expression of the B95-8 Epstein-Barr virus genome.";
 07-211(1984).

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CC	EMBL; V01555; -; NOT_ANNOTATED_CDS.
DR	PIR; A03742; Q0B03.
DR	Hypothetical protein; Early protein; Repeat.
DR	FW DOMAIN 149 648 4 X 125 AA TANDEM REPEATS.
KT	FT REPEAT 149 273 1.
FT	REPEAT 274 398 2.
FT	REPEAT 399 523 3.
FT	REPEAT 524 648 4.
FT	SEQUENCE 660 AA; 66244 MW; 86DA1D67A37152A2 CRC64;
SQ	

Query Match 2.9%; Score 172.5; DB 1; Length 660;
Best Local Similarity 26.1%; Pred. No. 0.0014;
Matches 94; Conservative 16; Mismatches 159; Indels 91;

167	AYQVC--GPLYQLGAATOQ--RPPPHASGPRRLGCERAWNHVSREAGVPLGLI	QY
244	AAQRCFAGPPPTRSGAAQRTHRPPGCPRSARNPGCPTWR---RSSGAQRGHI	Db
223	REGSASRLP-LPKRPRRGAAPP-ERTPVQCSWAHPGRTGRPSDRGFCV-V	QY
301	QRESGPTGGRPAAGAGCTPAAPGCGGAAVPFGATPHPERGSGFADPPAARLI	Db
278	-----PAEETSLEGAL-----SCG	QY
361	PRLPDOLAAQRCFAGPPPTRSGAAQRTHRPPGCPRSARNPGCPTWRRRSG	Db
298	SVGRQHAGPSTSRPPRW--DTPCPP-----VYAEKHLVYSGDKE---	QY
421	PRGAGQPSGTTGGRPAAGFAGPTPAAPGCGGAAVPFGATPHPERGSGFADPP	Db
343	PSFLSSLRPSLTGARRLVETIFLGSRRMPG-----TPRRLPRLPQ-----	QY
481	PERQERLPQDLAAQRCF-----AGPPPTRSGAAQRTHRPPGCPRSARNPGCF	Db
390	RLFLLELGNHAQCPYGVLLKTHCP-L--RAAVTAAAGVCAREKPGGVAAPGEEL	QY
537	RS-----GAQRGHPPPGAGQPSGTTGGRPAAGFAGPTPAAPGCGGAAVPFGAI	Db

RESULT 10	SF01 MOUSE	STANDARD;	PRT;	653 AA.
ID	SF01 MOUSE			
AC	Q64213; O08817; P70167; Q61454; Q92124;			
DC	15-MAR-2004 (Rel. 43, Created)			
DT	15-MAR-2004 (Rel. 43, Last sequence update)			
DDT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Splicing factor 1 (Zinc finger protein 162)			
DE	ZFMI (mzfm) (Zinc finger gene in MEN1 locus)			
DE	binding protein MBBP) (BBP) (CW17).			
DE	SF1 OR ZFP162 OR ZFMI.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu			
OC	NCBI_TaxID=10090;			
RN	[1]			
RRP	SEQUENCE FROM N.A. (ISOFORMS CW17 AND CW17E).			
RRP	STRAIN=C57BL/10; TISSUE=Spleen;			
RRP	MEDLINE=97355688; PubMed=9212169;			
RRP	Wrehlke C., Schmitt-Wrede H.-P., Qiao Z.D., Wunderlich F.;			
RRP	"Enhanced expression in spleen macrophages of the mouse homolog			
RRP	human putative tumor suppressor gene ZFMI.1";			
RRP	DNA Cell Biol. 16:761-767(1997).			
RRP	[2]			
RRP	SEQUENCE FROM N.A.			
RRP	STRAIN=C57BL/10;			
RRP	MEDLINE=99287587; PubMed=10360842;			
RRP	Wrehlke C., Wiedemeyer W.-R., Schmitt-Wrede H.-P., Mincheva A.,			
RRP	Lichter P., Wunderlich F.;			
RRP	"Genomic organization of mouse gene zfp162 (mzfm).";			
RRP				

1. 18:419-428 (1999).

M N.A. (ISOFORMS CML7E AND 3).
e; TISSUE-Breast tumor, and Osteoblast;
8257; PubMed12477932;
.L., Feingold E.A., Grouse L.H., Derge J.G.,
Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Jordan H., Moore T., Max S.J., Wang J., Hsieh F.,
Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
Quellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
lton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A., Touchman J.W., Green E.D., Dickson M.C.,
C., Grimwood J., Schmutz J., Myers R.M.,
Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schein J.E., Jones S.J.M., Marra M.A.;
and initial analysis of more than 15,000 full-length
use cDNA sequences.
Acad. Sci. U.S.A. 99:16899-16903 (2002).
: Necessary for the ATP-dependent first step of
ome assembly. Binds to the intron branch point sequence
-UACUAC-3' of the pre-mRNA. May act as transcription
r (By similarity).
Binds U2AF2. Interacts with U1 snRNA. Binds EWSR1, FUS
5 (By similarity).
LAR LOCATION: Nuclear.
IVE PRODUCTS:
ternative splicing; Named isoforms=3;
7;
264213-1; Sequence=Displayed;
7E;
264213-2; Sequence=VSP_050424;
264213-3; Sequence=VSP_008840;
3 experimental confirmation available;
PECIFICITY: Detected at intermediate levels in spleen,
vels in heart, kidney, brain, liver, testis, bone marrow,
gland, lymph nodes, pancreas and thymus.
phorylation on Ser-20 interferes with U2AF2 binding and
ome assembly (By similarity).
IV: Contains 1 CCHC-type zinc finger.
IV: Contains 1 KH domain.

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uires a license agreement (See <http://www.isb-sib.ch/announce/>
mail to license@isb-sib.ch).

; CAA56440.1; -;
; CAA59797.1; -;
; CAA70113.1; -;
; CAA73359.1; -;
91; AAH09091.1; -;
70; AAH55370.1; -;
5403; Zfp162.
R004087; KH dom.
R004088; KH_type.1.
R001878; Znf_CCHC.
3; KH; 1.
8; zf-CCHC; 1.
939; C2HCZNFINGER.
22; KH; 1.
43; Znf_C2HC; 1.
0084; KH_type_1; 1.

DR PROSITE: PS50158; ZF_CCHC; 1.
KW mRNA processing; mRNA splicing; Transcription regulation; Repres
KW Nuclear protein; Spliceosome; RNA-binding; Metal-binding; Zinc;
KW Zinc-finger; Phosphorylation; Alternative splicing.
FT DOMAIN 15 19 NUCLEAR LOCALIZATION SIGNAL (POTENT
KH.
FT ZN FING 141 222 CCHC-TYPE.
FT ZN FING 277 296 PRO-RICH.
FT DOMAIN 324 585 PHOSPHORYLATION (BY PKG) (BY SIMILA
FT MOD_RES 20 20 TTTTTSAGTSGIPPPWQQQAAAAAASPTGPGQGN
FT VARSPIC 529 653 PPGQPPPLPGAPPPPTSCIECLLSLSPNSLCL
RIPRSGDGPSEHEDFRLPLTLPGRQPQRPWW
AA -> SLPAAMARAMRVTRFAHW (in isof
CML7E).
FT /FTID=VSP_050424.
FT VARSPIC 586 653 TCSIECLLSLSPNSLCLSPNRAARIPRSGDGP
FRPLVTLPGRQPQRPWMTGWFVKAA -> PPPP
MYAPPPPPPPMDPSNFTVMGMGVAGMPFGMP
PQN (in isoform 3).
FT /FTID=VSP_008840.
FT CONFLICT 184 184 E -> K (IN REF. 3).
FT CONFLICT 509 509 P -> S (IN REF. 3; AAH55370).
FT CONFLICT 524 524 P -> L (IN REF. 3; AAH09091).
FT CONFLICT 528 528 N -> R (IN REF. 1).
SQ SEQUENCE 653 AA; 70408 MW; 8228DE3E79AB1BFC CRC64;

Query Match 2.5%; Score 150.5; DB 1; Length 653;
Best Local Similarity 22.5%; Pred. No. 0.036;
Matches 81; Conservative 26; Mismatches 148; Indels 105;

QY 163 APSCAVQVCGPPLYQLGAATQARPPHAGSPRRRLGCRANWHSVR-----EAG
Db 343 APRPAAPASNPPLPSLMTTQGRPPWMSGP-----SENRYHGMHGGGPGGPGG
QY 217 PAPGARRCGSASRLPLKRRPRGAAP--EPERTPVGGQSWAHGRTGSPDRG
Db 398 PHPLPSLTGGHGH--PMOHNPNGPPPPWMPQPPPPMNQ--PHPPGHHGPP---
QY 275 PARPAEATSLGALSGTRHSH-----PSVGRQHAGRPSTSRPPRPWDTPC
Db 446 ---PMDQYLGSTFVSGGVRLHQQGMMPPPWGMMPPPPPPPSGPL
QY 327 ETXKHFYSSGDKXQLR-----PSFLLSLRPSLTGARELVETIFLGS---RPMW
Db 500 -----WQQOQQQPPPPPPSSSMASSTPLWQNTTTTTSAGTSGIDPQW
QY 373 ----PCTPRRLPLQRYWQMPLELLGNHAQCPYGVLLKTHCPRLRAVTPAA
Db 551 AAASPGTP-----QMGNPTWVPLPFGVQVPLPPGAPPPPTC
QY 426 -----CAREKPGQSVAAPEEDTPRRLVQL--LRQHSPPQVY
Db 593 LCLLSLSPNSLCLSPNRAARIPRSGDGPSEHEDFRLPLTLPGRQPQRPWWTG

RESULT 11

MBD6 HUMAN
ID MBD6 HUMAN STANDARD; PRT; 1003 AA.
AC Q96DN6; Q8N3M0; Q8NA81; Q96Q00;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Methyl-CpG binding domain protein 6.
GN MBD6 OR KIAA1887.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,

[illegible]

TY: Contains 1 myosin-like globular head domain.

TY: Contains 1 FERM domain.

TY: Contains 2 IQ domains.

TY: Contains 1 MYTH4 domain.

TY: Contains 1 SH3 domain.

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95; AAF05904.1; -

30; AAC40124.1; -

10; BAA36582.1; -

A59295.

T42386.

; 1BR2.

1811; Myo15.

R000299; Band 4.1.

R000048; IQ region.

R001609; myosin_head.

R000857; MYTH4.

R001452; SH3.

2; IQ; 2.

3; myosin_head; 1.

4; MYTH4; 2.

193; MYOSINHEAVY.

0355; myosin_head; 1.

95; B41; 1.

15; IQ; 2.

42; MYSC; 1.

39; MYTH4; 2.

26; SH3; 1.

0096; IQ; 2.

0002; SH3; 1.

0660; FERM_1; FALSE_NEG.

0661; FERM_2; FALSE_NEG.

0057; FERM_3; 1.

binding; Actin-binding; Coiled coil; Repeat; SH3 domain;

tion; Deafness.

1 1871 MYOSIN HEAD-LIKE.

872 2013 NECK OR REGULATORY DOMAIN.

014 3511 TAIL.

307 1334 COILED COIL (POTENTIAL).

776 1783 ACTIN-BINDING (POTENTIAL).

886 1908 IQ 1.

909 1938 IQ 2.

848 2934 SH3.

190 3511 FERM.

299 1306 ATP (POTENTIAL).

779 1779 C -> Y (IN SH2).

330 1331 MISSING (IN REF. 2).

579 1579 L -> R (IN REF. 3).

955 1972 MISSING (IN REF. 2).

077 2077 L -> M (IN REF. 2).

139 2139 L -> P (IN REF. 2).

953 2953 V -> A (IN REF. 2).

511 AA; 395533 MW; 38C962F98A2D395B CRC64;

2.4k; Score 144; DB 1; Length 3511;

larity 17.6k; Pred.No. 0.79;

Conservative 117; Mismatches 385; Indels 380; Gaps 44;

RCRAVRLSHRYEVLPLATFVRLGPGQWRLVQRGDPAAFRALVAQCILVCP---59

RLASPGSLRQH-----PPFW-----AAPAHVPPPOA 707

DARPPPPAA-----PSFRQVSLKELVARVLQRLCERGAKNVLAFGFA 102

3FAEPPGTSVEAPDLLAFVPPPSFR-----ASRSRRAAYGFP 751

103 LLDGARGPPEAFTTSVRSYLPNTVTD--ALRGSGAWGLLRVGGDDVAVHLLAI
752 -----SPLIGSRRRPHLPSPQPSLRSLPQQ-----
161 LVAPSCAYQCGPPLQLGAATQARPSPHASGPRRLGGERAWNHSVREAGVPLC
779 -----YHSLGSLPLSLRRRGPFPQPPPPRRPQSLREAF--SLRRASGRIG
216 -----LPAGARRRGSASRSLPKR-----PRGAAPERT---F
831 VLGSPPPPPPKLGKPHRSNLPSRLPRTWRRLSEPPEPTRAVKPMVHRAYPPE
256 WAHPGTRGTRGDFCVWSPARPAEATSLGALSGTRHSHPSVGRQHAGPPST
891 W---GASTGALE-----QQENQREADETPTWTPVPLAPSWDVMDEPT
316 PWDTPC-----PPVYAEKHFLYSS-----GKKEQLRE
936 PMPEGIGSLRGFSRPPVPENPLEHTSPSCPEQSEDVSNLTGIFLGQHDHDPGE
349 SLRPSLTGARRLVETIFLGSRRPMWPGTPRRL--PRLPQRYWQMPLELLGNH--
996 SADPSL---EKPEEVVTLGD--POPPAEPEALNTPPNKNVSVSEKVLRLSASVPI
401 --AQCP---YGVLLKTHCPRAAATPAAGVCAREKPOGS-----
1052 ARATWQPMHRKIVSETPAPLAPTRAPGPLLKAGEQPAEPGRFAVMPQVRGVS
435 ---VAPEEEDTPRR-----LVQLLRHSSPMQVYG
1112 GPAPVQPPHDPQDPQGPAPQACSLRWPCMLWPPPTDAHCLWSIRTYSSQSHLRG
469 LRRL---VPPGLWGRHNRERRFLNTKFLSLGKHAKLSIQELTWKMSVDCAWL
1172 HKSLWKTRPSW---ONKHSIRNLPMSRREQHRDGVEDMTQLEDLOETTVL
526 VGCVPAAEHRLREILAKFL-----HVLMSVYVVELLSRF-----
1226 -----LKTRFERNLITYIGSILSVNPNYRMPAIYGPQVQVQSGRAGENPPH
565 ETTFQK-----NRLFFYR-----KSVWSKL-----QSIGRQHLKRVQL
1280 NLAFAKMLDAKONQCVIIISGESGSGTEATKLILRLCLAAMNQRRDVMQKILEA
604 A-----EVROHREARPALTSRLRFTPKDGLRPIVNDYVVGARTFREKRAER
1340 AFGNAKTVRDSSR---FGKVEIFLEGVIGCAITSQYLLEKSRIVFOAKNER
654 -----LTSRVKALFSVLNVE-----RARRPGLLGASVLGLDDIHRAWRTFVLR
1397 YELLAGLPAQLRAQAFSLQEAETVYVLNQGNCIEAGKS--DADDPR-----
702 PPELYFVKVVDVTGAYDTIPQDLREVIASIIKPNQTYCVRRYAVVQKAAHGHVR
1442 -----LLAAEVLIG-FTSEDQDSIFRILASILHLGNVYFEKHETDAQEVA-----
762 HYSTLTDLQPMYRQFVAHLQETSP--LRDAVVIQSSSLNEASSGLFDVFLRMC
1486 SVVSAREIOA-----VAELLQVSPGLQKAITFKVTEIRE-----KIFTELTV
820 IRGKSVQCGIPIQSGSIILSTLCSCYGD MENKLFAGI--RRDGLLLRLVD 868
1535 AR-----DATAKVLVALLFGWLITRVNALVSPKQDTLSIALD 157.

RESULT 13

IE18_PRIVIF

ID IE18_PRIVIF

AC P11675;

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 01-FEB-1994 (Rel. 28, Last annotation update)

early protein IE180.

virus (strain Indiana-Funkhauser / Becker) (PRV).
DNA viruses, no RNA stage; Herpesviridae;
Varicellinae; Varicellovirus.

1523;

OM N.A.

15207; PubMed=2546124;

side sequence analysis of the immediate-early gene of
virus";
is Res. 17:4637-4646(1989).

MOV-1989) to the EMBL/GenBank/DBJ databases.

THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE
TING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING
RAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.

EAR LOCATION: Nucleus of infected cells.
ong stretch of serine residues may be a major site of
ylation.

TY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.

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mail to license@isb-sib.ch).

CAA33214.1;

EDBEIF.

R005205; Herpes ICP4 C.

R005206; Herpes-ICP4_N.

5; Herpes-ICP4_C; 1.

4; Herpes-ICP4_N; 1.

n; Transcription regulation; Trans-acting factor;

Phosphorylation; Nuclear protein.

390 405 POLY-SER.

958 966 POLY-SER.

461 AA; 149833 MW; 7F31E7ABE403E208 CRC64;

larity 2.4%; Score 142; DB 1; Length 1461;

Conservative 23.9%; Pred. No. 0.35;

Mismatches 158; Indels 172; Gaps 28;

ALVAQCLVCVWDARPPAPSPROVSCIKELVARVLQICRGAKNVLAFGFALLD 105

3VLERLLPC-FLRLPAPAPAPALGPACLEEVTAALL-----ALRD 746

3-GPPE-----AFTTSVRSVLPNTVTDALRGSGAWGLLRVCDVILHLLAR 155

JAGPAERQQAADSVLVARVAVLVRSVDCARAEAM-----TYA 791

TVLVASCAVQVGPPLYLQGAATQAPPPHPSGRRRLGCRANWH-----S 206

-----APA-----NVAGARL-----AEAAAFPGPAEPAP-----GLPLMPEQGLVVPAPA 837

AGVPLGLPAGP-----ARRRGGSASRLPLPK-----RPRGAAPPEPTV 251

AGAPGLFGGPGSPASTKSGSTKSSGKSLGSSGYASSFAAGPDPAPER--- 894

3MAHPQRTGRPSDRGFCVSPAPR---AEEATSLEG-ALSTSHSHPSVGRQHAGPP 308

---RKXKRAPGAR-----RPGGEDEGLSGALRDGDGHGRD--DEEDRGR 938

IP-----PRWDTPCPVPYATKHYLYSGDKQLRPSFLISSLRPSLTGARRLVETI 364

ISLGLGPAP--DPAPALVSSSSS--SSSSEDDRLR-----RP----- 974

QY 365 FLGSRPMWPGTPRRLPRLPQRYWQWRPLFLELLGNHQAQCPYGVLLKTHCP-----
Db 975 -LGMPEHPADGGRRRVPAG-----ETHTRPSAAALAAAYCPPEVA
QY 415 -----LRAAVT--PA--AGVCAREKPKQGSVAAPPEEDTPRRLVQLLRQHSPP
Db 1022 EVFPELWRPALTFDPAALAHIAAR--RGAAGAP-----LRRRAAWNRQIADP

RESULT 14

IF2 BORPE

ID IF2 BORPE STANDARD; PRT; 997 AA.

AC Q7VYR2;

DT 15-MAR-2004 (Rel. 43, Created)

DT 15-MAR-2004 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Translation initiation factor IF-2.

GN INFB OR BP1247.

OS Bordetella pertussis.

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Alcaligenaceae; Bordetella.

OX NCBI_TaxID=520;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;

RX MEDLINE=22827954; PubMed=12910271;

RA Parkhill J., Sebathia M., Preston A., Murphy L.D., Thomson N.,

Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungai

Cardeno-Farraga A.M., Temple L., James K., Harris B., Quail M.A.

Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jegelis

Leather S., Moulé S., Norbertczak H., O'Neill S., Ormond D., Price

Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Steve

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,

"Comparative analysis of the genome sequences of Bordetella pert

Bordetella parapertussis and Bordetella bronchiseptica.";

Nat. Genet. 35:32-40(2003).

CC -!- FUNCTION: One of the essential components for the initiator

protein synthesis. Protects formylmethionyl-tRNA from sponta

hydrolysis and promotes its binding to the 30S ribosomal sub

Also involved in the hydrolysis of GTP during the formation

70S ribosomal complex (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: Belongs to the IF-2 family.

CC This SWISS-PROT entry is copyright. It is produced through a col

between the Swiss Institute of Bioinformatics and the EMBL ou

the European Bioinformatics Institute. There are no restrictio

use by non-profit institutions as long as its content is i

modified and this statement is not removed. Usage by and for

entities requires a license agreement (See <http://www.isb-sib.ch>

or send an email to license@isb-sib.ch).

CC EMBL; BX640414; CAE41543.1; --

DR HAMAP; MF_00100; -- 1.

DR InterPro; IPR004161; EFTU_D2.

DR InterPro; IPR000795; EF_GTPBind.

DR InterPro; IPR000178; IF2.

DR InterPro; IPR006847; IF2_N.

DR InterPro; IPR005225; Small_GTP.

DR Pfam; PF00009; GTP_EFTU_1.

DR Pfam; PF03144; GTP_EFTU_D2; 2.

DR Pfam; PF04760; IF2_N; 2.

DR ProDom; PD186100; IF2; 1.

DR TIGRFAMs; TIGR00487; IF-2; 1.

DR TIGRFAMs; TIGR00231; small_GTP; 1.

DR PROSITE; PS01176; IF2; 1.

KW Initiation factor; Protein biosynthesis; GTP-binding;

Complete proteome.

FT DOMAIN 501 649

NP_BIND 507 514

G-DOMAIN.

GTP (BY SIMILARITY).

STANDARD; PRT; 623 AA.

```
(Rel. 42, Created)
(Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
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355;

5157; PubMed=12617815;

nopus Deltex homologue expressed in diff

attn: 2:283-287(2002).

in cell-cell communication

and negative regulator of Notch, depending on the

protein for the Notch pathway (By similarity).

May form a homo- or heteromultimer with other members of ex family. Probably interacts with Notchl (By similarity). **PECIFICITY:** Specifically expressed in regions undergoing differentiation. Mainly colocalizes with Notchl. **FUNCTIONAL STAGE:** In the tailbud stage, it is expressed in the

DR EMBL; AJ431211; CAD26517.1; -.

DR InterPro; IPR001841; Znf_ring.

DR SMART; SM00678; WWE; 2.

DR PROSITE; PS00518; ZF_RING_1; F

KW Repeat; Metal-binding; Zinc; Z

FT	DOMAIN	WT
FT	DOMAIN	170

FT	DOMAIN	226	243
FT	DOMAIN	226	243

[illegible]

Query Match
Best Local Similarity 25.68%

Matches 101; conservative 35;

QY I/Z GPFLYQLGAATQARPPPP--HA

Db 228 GPP-----PALPPPPPIHP

QY 227 SASRSLFLPKRPRRGAAPEPE

Db 277 GFSRSQSVP-----GAAPYP-

285 LEGAL SCIENCE AND POLICY

[illegible]

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QY 334 336 338 340 342 344 346 348 350 352 354 356 358 360 362 364 366 368 370 372 374 376 378 380 382 384 386 388 390 392 394 396 398 400 402 404 406 408 410 412 414 416 418 420 422 424 426 428 430 432 434 436 438 440 442 444 446 448 450 452 454 456 458 460 462 464 466 468 470 472 474 476 478 480 482 484 486 488 490 492 494 496 498 500 502 504 506 508 510 512 514 516 518 520 522 524 526 528 530 532 534 536 538 540 542 544 546 548 550 552 554 556 558 560 562 564 566 568 570 572 574 576 578 580 582 584 586 588 590 592 594 596 598 600 602 604 606 608 610 612 614 616 618 620 622 624 626 628 630 632 634 636 638 640 642 644 646 648 650 652 654 656 658 660 662 664 666 668 670 672 674 676 678 680 682 684 686 688 690 692 694 696 698 700 702 704 706 708 710 712 714 716 718 720 722 724 726 728 730 732 734 736 738 740 742 744 746 748 750 752 754 756 758 760 762 764 766 768 770 772 774 776 778 780 782 784 786 788 790 792 794 796 798 800 802 804 806 808 810 812 814 816 818 820 822 824 826 828 830 832 834 836 838 840 842 844 846 848 850 852 854 856 858 860 862 864 866 868 870 872 874 876 878 880 882 884 886 888 890 892 894 896 898 900 902 904 906 908 910 912 914 916 918 920 922 924 926 928 930 932 934 936 938 940 942 944 946 948 950 952 954 956 958 960 962 964 966 968 970 972 974 976 978 980 982 984 986 988 990 992 994 996 998 1000

DD 378 VSGICRAIKNCHLNSANPEE

Qy 384 QRYWQMRPLFLELLGNHAQC-

Db 433 -----RGIRAEIVGKLGKCN

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100

DB 475 AIYGEKTGTQPPGKMEF---H

Qy 492 KKFISLG--KHAKLSLQELTWN

Db 527 KKFTARGFPRHCYLPDNDKGRN

Search completed: April 22, 2004, 00:00

GenCore version 5.1.6
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main search, using sw model

April 21, 2004, 23:41:41 ; Search time 83 Seconds
(without alignment)
4303.212 Million cell updates/sec

IS-09-424-686F-2

MPRAPRCRAVRLSHRYRE.....TALEAAANPALPSDFKTILD 1132

LOSUM62

apop 10.0 , Gapext 0.5

017041 seqs, 315518202 residues

its satisfying chosen parameters: 1017041

ngth: 0

ngth: 2000000000

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

SPREMBL_25.*

```
: sp_archaea.*
: sp_bacteria.*
: sp_fungi.*
: sp_human.*
: sp_invertebrate.*
: sp_mammal.*
: sp_mmc.*
: sp_organelle.*
: sp_phage.*
0: sp_plant.*
1: sp_rodent.*
2: sp_virus.*
3: sp_vertebrate.*
4: sp_unclassified.*
5: sp_rvirus.*
6: sp_bacteriap.*
7: sp_archaeap.*
```

s the number of results predicted by chance to have a
er than or equal to the score of the result being printed,
ved by analysis of the total score distribution.

SUMMARIES

Query	Length	DB	ID	Description
93.7	1069	4	Q8NG46	Q8NG46 homo sapien
68.0	807	4	Q8N6C3	Q8N6C3 homo sapien
66.6	795	4	Q8NG38	Q8NG38 homo sapien
60.9	1128	11	Q9QXZ4	Q9QXZ4 mesocricetu
47.4	524	4	Q9UBR6	Q9UBR6 homo sapien
38.9	1191	13	Q9DB32	Q9DB32 xenopus lae
37.0	523	4	Q94807	Q94807 homo sapien
33.8	575	11	Q9JK99	Q9JK99 ratus norv
23.0	514	11	Q9R266	Q9R266 mus musculu
12.2	1123	10	Q9SE99	Q9SE99 arabidopsis
12.2	1123	10	Q9SPU7	Q9SPU7 arabidopsis
11.5	1259	10	Q9AU13	Q9AU13 oryza sativ
11.0	1261	10	Q8LKW0	Q8LKW0 oryza sativ
8.0	1032	5	Q7Z1L1	Q7Z1L1 euploies cr
8.0	1032	5	Q8MUB3	Q8MUB3 euploies cr
7.5	85	4	Q9UNS6	Q9UNS6 homo sapien

17	449	7.5	116	11	Q80SU5	Q80SU5 r
18	441	7.4	1032	5	Q7Z1L0	Q7Z1L0 eu
19	408	6.8	823	5	Q8SQ00	Q8SQ00 en
20	397	6.7	104	11	Q9JLM1	Q9JLM1 m
21	395.5	6.6	1135	5	Q818Z7	Q818Z7 st
22	394	6.6	73	4	Q9UNR4	Q9UNR4 ho
23	392	6.6	1108	5	Q818Z6	Q818Z6 st
24	365	6.1	867	3	Q9P8T3	Q9P8T3 ca
25	364	6.1	895	5	Q9GRCS	Q9GRCS pa
26	361	6.1	867	3	Q9P8T2	Q9P8T2 ca
27	342	5.7	896	5	Q8MUQ8	Q8MUQ8 pa
28	339	5.7	79	6	Q7YR69	Q7YR69 fe
29	200	3.4	52	11	Q9ROB3	Q9ROB3 m
30	188.5	3.2	960	5	Q9NCP5	Q9NCP5 gl
31	179	3.0	2675	2	Q9PB23	Q9PB23 st
32	167	2.8	1474	5	Q962P9	Q962P9 cr
33	161	2.7	1070	4	Q96JG5	Q96JG5 hor
34	159	2.7	771	10	Q9XHY4	Q9XHY4 O
35	152.5	2.6	296	12	Q69118	Q69118 h
36	152	2.5	1285	10	Q9LWK0	Q9LWK0 o
37	151.5	2.5	539	10	Q9SR71	Q9SR71 ai
38	151.5	2.5	669	4	Q8N4X0	Q8N4X0 hor
39	150.5	2.5	653	11	Q08817	Q08817 m
40	150	2.5	611	11	Q8KOM8	Q8KOM8 m
41	150	2.5	850	11	Q9JL15	Q9JL15 m
42	150	2.5	850	11	Q8OXI6	Q8OXI6 m
43	148.5	2.5	1305	11	Q8OYF9	Q8OYF9 m
44	147.5	2.5	986	12	Q9DW99	Q9DW99 r
45	147	2.5	1186	12	Q7T401	Q7T401 s

ALIGNMENTS

RESULT 1

```
Q8NG46
ID Q8NG46 PRELIMINARY; PRT; 1069 AA.
AC Q8NG46;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Telomerase reverse transcriptase.
GN HTER.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hisatomi H., Nagao K., Hirata H., Hikiji K., Kanamaru T.;
RT "Exon 11 deleted variant of the human telomerase reverse
transcriptase."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB085628; BAC11010.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0003721; F:telomeric template RNA reverse transcripts.
DR InterPro; IPR003545; Telomerase_RT.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 1069 AA; 120047 MW; BE1E77A653B1C666 CRC64;
```

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Query Match 93.7%; Score 5583.5; DB 4; Length 1069;
Best Local Similarity 94.4%; Pred. No. 0;
Matches 1069; Conservative 0; Mismatches 0; Indels 63;

QY 1 MPRAPRCRAVRLSHRYREVLPLATFVRRLGPGQWRVQRGDPAAFRALVAQCL
Db 1 MPRAPRCRAVRLSHRYREVLPLATFVRRLGPGQWRVQRGDPAAFRALVAQCL
QY 61 DARPPPAAPSFRQVCLKELVARVLQRLCERGAKNVLAFGFALLDGGAGPPPAF
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AEVQHREAPALATSLRIFPKDGLRPINMDDVVGARTFRKRAERLTSRVKA 660

VLNYERARRPGLIGASVLGLDDIHRAMKTFVLVRQAOPPPPELYFKVDVTGAYDTI 720

VLNYERARRPGLIGASVLGLDDIHRAMKTFVLVRQAOPPPPELYFKVDVTGAYDTI 720

RLTEVIASIIKPONTYCVRRYAVVQKAAHGHRKAFKSHV 763

RLTEVIASIIKPONTYCVRRYAVVQKAAHGHRKAFKSHV 763

PRELIMINARY; PR; 795 AA.

(T:EMBLrel. 22, Created)

(T:EMBLrel. 22, Last sequence update)

(T:EMBLrel. 25, Last annotation update)

variant of telomerase reverse transcriptase.

(Human).

stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Primates; Catarhini; Hominidae; Homo.
606;

M. N. A.
ch;
Nagao K., Kanamaru T., Hizata H., Miyachi K., Hikiji H.;
JN-2002) to the EMBL/GenBank/DBJ databases.
50; BAC11015.1; -;
34; C.nucleus; IEA.
77; F.DNA binding; IEA.
64; F.RNA-directed DNA polymerase activity; IEA.
21; F.telomeric template RNA reverse transcriptase. .; IEA.
3003545; Telomerase_RT.
365; TELOMERASERT.
DNA polymerase.
95 AA; 88965 MW; 6BEAC8A6D1A2E8CB CRC64;
66.6%; Score 3973; DB 4; Length 795;
arity 98.4%; Pred. No. 2.4e-298;
Conservative 0; Mismatches 0; Indels 12; Gaps 1;
APRCRAVRSLLRSHYREVLPATFVRLPGQWRLVQGDPAAPRALVAQCLVCVPW 60
APRCRAVRSLLRSHYREVLPATFVRLPGQWRLVQGDPAAPRALVAQCLVCVPW 60
PPAAPSPQVSCLELVARVLQRLCERGAKNVLAFGALLDARGGPPPEAFTTSVR 120
PPAAPSPQVSCLELVARVLQRLCERGAKNVLAFGALLDARGGPPPEAFTTSVR 120
NTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
NTVTDALRGSGAWGLLLRRVGGDVLVHLLARCALFVLVAPSCAYQVCGPPLYQLGA 180
RPPPHASGPRRLGGERAWNHVREAGVPLGLPAPGARRRGGSASRLPLPKPRR 240
RPPPHASGPRRLGGERAWNHVREAGVPLGLPAPGARRRGGSASRLPLPKPRR 240
BPERTPVQGSWAHPGRTGSPDRGFCVVSPPARPEAETSLEGALSGTRHSHPSVG 300
BPERTPVQGSWAHPGRTGSPDRGFCVVSPPARPEAETSLEGALSGTRHSHPSVG 300
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IAGPPTSPRPPDWTCPVPVYAEKHFLYSSGDKEQLRPSFLSLTGARRL 360
FLGSPRPMWGGTPRRLPLRPLQRYQWRPLFLELLGNHAQCPYGVLLKTHCPLRAV 420
FLGSPRPMWGGTPRRLPLRPLQRYQWRPLFLELLGNHAQCPYGVLLKTHCPLRAV 420

Qy	421	PAAGVCAREKPGQSGVAAPEEEDTDPRRLVQLLRQHSPPWQVYGFVRACLRLRLVPI	
Db	421	PAAGVCAREKPGQSGVAAPEEEDTDPRRLVQLLRQHSPPWQVYGFVRACLRLRLVPI	
Qy	481	RHNERFLNTYKTFISLGHAKHLSLQELTWKQSVVRDCAWLRSSPGVGCVPAAEHH	
Db	481	RHNERFLNTYKTFISLGHAKHLSLQELTWKQSVVRDCAWLRSSPGVGCVPAAEHH	
Qy	541	LAKFLHLMSSVVVVELLSRFFVVTETTFQKNRLFYRKSVMSKLOSTIGTQHLKF	
Db	541	LAKFLHLMSSVVVVELLSRFFVVTETTFQKNRLFYRKSVMSKLOSTIGTQHLKF	
Qy	601	LSEAEVQRHREARPALLTSRLRFIPKPDGLRPINVMMDYVVGARTFRREKKAERLI	
Db	601	LSEAEVQRHREARPALLTSRLRFIPKPDGLRPINVMMDYVVGARTFRREKKAERLI	
Qy	661	LFSVLNYESAREPGLLGASVILGLDDIHRAMTFVLRVRAQDPPELYFVKVDVTC	
Db	661	LFSVLNYESAREPGLLGASVILGLDDIHRAMTFVLRVRAQDPPELYFVKVDVTC	
Qy	721	PODRLETVIASIIKPNQTYCYRRVAVVQKAAGHVRKAFKSHV 763	
Db	711	--DRLETVIASIIKPNQTYCYRRVAVVQKAAGHVRKAFKSHV 751	
RESULT 4			
Q9QXZ4			
ID	Q9QXZ4	PRELIMINARY;	PRT; 1128 AA.
AC	Q9QXZ4		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Telomerase catalytic subunit.		
OS	Mesocricetus auratus (Golden hamster).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;		
OC	Mesocricetus.		
NC	NCBI_TaxID=10036;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE-21240330; PubMed=11342218;		
RA	Guo W., Okamoto M., Lee Y.M., Baluda M.A., Park N.H.;		
RT	"Enhanced activity of cloned hamster TERT gene promoter in trans		
RT	cells";		
RL	Biochim. Biophys. Acta 1517:398-409(2001).		
DR	EMBL; AF149012; AAF17334.1; -		
DR	GO; GO:0005634; C:nucleus; IEA.		
DR	GO; GO:0003677; F:DNA binding; IEA.		
DR	GO; GO:0003723; F:RNA binding; IEA.		
DR	GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.		
DR	GO; GO:003721; F:telomeric template RNA reverse transcriptase.		
DR	GO; GO:0016740; F:transferase activity; IEA.		
DR	GO; GO:0006278; P:RNA dependent DNA replication; IEA.		
DR	InterPro; IPR000477; RVase.		
DR	InterPro; IPR003545; Telomerase_RT.		
DR	Pfam; PF00078; rvt; 1.		
DR	PRINTS; PR01365; TELOMERASERT.		
KW	RNA-directed DNA polymerase; Transferase.		
SQ	SEQUENCE 1128 AA; 128334 MW; 1D4F81249012174E CRC64;		
Query Match			
Best Local Similarity 60.9%; Score 3628; DB 11; Length 1128;			
Matches 736; Conservativity 124; Mismatches 238; Indels 64; C			
Qy	1	MPRAPRCRAVRSLLRSYRVLPLATFVRRLGPGQWRVLVQRGDPAAFRALVAQCLV	
Db	1	MPRAPRCRAVRLRSQYRWFLATFVRRLGPGQWRVLVQRGDPAAFRALVAQCLV	
Qy	61	DARPPAAPSPFVSCLELVAVLQRLCERGAKNVLAFGFALLDGGAGSGPEAF	
Db	61	DSQPPADLGFHQVSSLUKELVAARVQRLCERGERNVLTFGFALLNGAAGSGPMTF	
Qy	121	SYLPTNTVDALRSGAGMLLRVRGDDVLVLLHLLARCALFVLVAPSCAVQVCGPPL	

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PNSVTSLSRVSGAWMLLNVRVGDLLVLLARCALYLLVPSPCAVQVCGSPLQICA 180
ARPP-PHASPFRRLG-----CERAWHNSVREAGVPLGLPAPGARRGGGASRS 231
TWSVSRIYPTVPVGNFTHLGSFTHVRNSSHQEAWKPPPLPSREAKRSLSTNRS 240
PKPRRGAAPERTPVQGSWAHPGTRGSDRGFCVVSPPAR-----PAEAEATSLG 287
SKKARCDLAPRLEKGPYRQA-----VPTPSDKTM-VPNPAKSHAVPISTIK-ED 291
GTRHSHSVGRQ-----HHAQPPSTS-RPP-----RPWDTCPVPVYATKHFPLVS 334
GVK--APGLSRSGSVCKYKRPSTSLQSPCLQNAFQLRP-----YTETKFLYS 341
DKEOLRSPFLLSSRLPGLTARRLVETIFLGSPPMMEGTFRRLPRLPORVWQRELF 393
GREELNPSFLNNLOPSLTGARRVLELFGMPRTSGGCGRRRLSKRWQWRPLF 401
LGHNAQCPYGVLLKTHCPRAAATPAAGVVCAREKPGQSVAAPEEEDTPRRLVQLLR 453
LVNHARCPYVLLRSHCRFRTAAHQVAGAL-----NTTSPQRLANLLR 447
SPQVQVCFVZACLRLLVPPGLWGRSHNRERFLNTKKFISLGKHAKLSLOELTWKMS 513
SPQVQVGFLOACVGLVPPGLWGRSHNRERFFKNVRFISLGKYDKLSLOELTWKMK 507
CWLRLSPGVGCVPAABHRLEETILAKFHLWMSVYVVELLSFFVYVTEFTFOKNRL 573
CWLRLSPGNNCPVAAEHRTRELLAVFLFWLMDAYVVELLSFFVYVTEFTFOKNRL 567
RKSWMSKLSIGIROHLKRVOLRSELSAEVROHREAPALLTSRLRPIKPDGLRPI 633
RKSWMRRLQSIGVRHLELVRVQLSQQEVRQEQEAMPAMPIKLRPIKPSGLRPI 627
DYVVGARTFPRKAEELTSRVKALPSVLYERARPPGLLGASVLGDLDDHRAWRTF 693
SY-MGTRAFDKGQAQHTQCLKTLFSLVNYELTKTNLGLASVLGDLNLYRTWRTF 686
VRAQDPPELVYFVKVDVTGAYDITPQDLRLTEVIAIIK-PONTYCVRYAVVOKAAH 752
VRLDPAFRMYFVKADVTGAYDAIPQDKLVEVIANWIRHPDINSYCHQYAVQDRQ 746
RKAFKSHVSTLTLQPMYRFVHAHQ--ETSPILRDVAVVIRQSSSLNEASSGLDFVL 810
IKSPFRQVSTLSDLPQHMGGFLKHLQSDTSALRNSVWIEQSLSLNEASSSLDFDL 806
JHAVAIRKSYVQCOGIPQGSILSTLLCSLCYGDMMENKLPAGIRRDGLLLRLVDDP 870
RNSVWIKIGRCYVQCOGIPQGSILSTLLCSLCFGDMENKLPFAEVQDGLLLRFVDDP 866
TPHLTHAKTFLRTLVRGVEYGCVMNLRKTVVNFVVEDEALGGTAFVQMPAHGLFPW 930
TPHLVQAEALRALVRGIPYGCVMINLQKTVVNFVVDAGTLDGTAHQHCLFPW 926
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LDTQTLVLCYDTGYARTSIKASLTQRTFKAGRNMRQKLLAVLAKCHSLFDLQ 986
JQVTCNIVKILLQAYRFHACVLQLPFHQVWKNPTFFLRVISTASLCYSILKAK 1050
JQVTCNIVKIFLLQAYRFHACALQLPFDQHKVKNPAFFLSIISNTASCYSILKVK 1046
KSLGAKGAAGLPSEAVQWLCHQAFLLKLRHRTVYVPLIGSLRTAQTLRKLPGT 1110
WTLKAKGASSGFPEPAARWLCYQAFLLKLAGHSVYTKLLGRLTAQKQLKLPRA 1106
ALSAANPALPSDFKTILD 1132
ILETAADPALSTDFQITILD 1128

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Q9UBR6
ID Q9UBR6 PRELIMINARY; PRT; 524 AA.
AC Q9UBR6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Telomerase reverse transcriptase (Fragment).
GN TERT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99144726; PubMed=10022128;
RA Greenberg R.A., O'Hagan R.C., Deng H., Xiao Q., Hann S.R., Adams
RA Lichtenstein S., Chin L., Morin G.B., Depinho R.A.;
RT "Telomerase reverse transcriptase gene is a direct target of c-M
RT is not functionally equivalent in cellular transformation.";
RL Oncogene 18:1219-1226(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99140777; PubMed=9988278;
RA Wu K.J., Grandori C., Amacker M., Simon-Vermot N., Polack A.,
RA Lingner J., Dalla-Favera R.;
RT "Direct activation of TERT transcription by c-MYC.";
RL Nat. Genet. 21:220-224(1999).
DR EMBL; AF121948; RAD24464.1; -
DR EMBL; AF114847; AD17210.1; -
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
KW RNA-directed DNA polymerase.
FT NON TER 524
SQ SEQUENCE 524 AA; 57932 MW; 5F47DEFD01832B1B CRC64;

Query Match 47.4%; Score 2825; DB 4; Length 524;
Best Local Similarity 100.0%; Pred. No. 8.2e-210;
Matches 524; Conservative 0; Mismatches 0; Indels 0;

QY 1 MPAPRCRAVRSLLSHREVLPATFVRLPGQGRVLRVQGDPAAFRALVQCL
DB 1 MPAPRCRAVRSLLSHREVLPATFVRLPGQGRVLRVQGDPAAFRALVQCL
QY 61 DARPPAAPSPQVSCLELVARVQLRCERGAKNVLAFFGALLDGARGPPEAF
DB 61 DARPPAAPSPQVSCLELVARVQLRCERGAKNVLAFFGALLDGARGPPEAF
QY 121 SYLPNTVTDALRGSGAWGLLIRVGGDVLVHLLARCALFVLVAPSCAYVCGPPL
DB 121 SYLPNTVTDALRGSGAWGLLIRVGGDVLVHLLARCALFVLVAPSCAYVCGPPL
QY 181 ATQARPPPHASGPRRLGGERAWNSVREAGVPLGLPAPGARRGGGASRSPLP
DB 181 ATQARPPPHASGPRRLGGERAWNSVREAGVPLGLPAPGARRGGGASRSPLP
QY 241 GAAPPERTPVQGSWAHPGTRGSDRGFCVVSPPARPAEATSLGALSGTRHSI
DB 241 GAAPPERTPVQGSWAHPGTRGSDRGFCVVSPPARPAEATSLGALSGTRHSI
QY 301 ROHAGAPSTSPRPWDTPCPVVAETKHFLYSSGDKQLRPSFLLSLRSLT
DB 301 ROHAGAPSTSPRPWDTPCPVVAETKHFLYSSGDKQLRPSFLLSLRSLT
QY 361 VETIFLGRPMWPGTFRRLPRLPQRYWQWRPLFLELLGNHQAQCPYGVLLKTHCP
DB 361 VETIFLGRPMWPGTFRRLPRLPQRYWQWRPLFLELLGNHQAQCPYGVLLKTHCP
QY 421 PAAGVCAEKPGQSVAAPEEEDTPRRLVQLLRQHSPPQVYGFVRACLRLVPPK
DB 421 PAAGVCAEKPGQSVAAPEEEDTPRRLVQLLRQHSPPQVYGFVRACLRLVPPK
QY 481 RHNERFLNTKKFISLGKHAKLSLOELTWKMSVRDCAWLRRSP 524
DB 481 RHNERFLNTKKFISLGKHAKLSLOELTWKMSVRDCAWLRRSP 524

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	PRELIMINARY; PRT; 1191 AA.	
(TREMBlrel. 16, Created)		
(TREMBlrel. 16, Last sequence update)		
(TREMBlrel. 25, Last annotation update)		
reverse transcriptase.		

is (African clawed frog).

- Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
- Tetrachia; Anura; Mesobatrachia; Pipidae; Xenopus.
- Xenopus.
- 355;

M N.A.
Ishikawa F.;
reverse transcriptase of Xenopus laevis";
JEC-1999) to the EMBL/GenBank/DDBJ databases.
.99; AAG43537.1;
34; C:nucleus; IEA.
.77; F:DNA binding; IEA.
23; F:RNA binding; IEA.
64; F:RNA-directed DNA polymerase activity; IEA.
21; F:tellomeric template RNA reverse transcriptas. . ; IEA.
40; F:transferase activity; IEA.
78; F:dna dependent dna replication; IEA.
R000477; RVTse.
R003545; Telomerase_RT.
8; rvt; 2.
365; TELOMERASE RT
DNA polymease; Transferase.
191 AA; 138016 MW; 98D9D776869A57D6 CRC64;

larity 38.4%; Score 2316.5; DB 13; Length 1191;
Pred No. 5.6e-170;
Conservative 201; Mismatches 381; Indels 123; Gaps 25;

APCRVRSLLRHSHYREVLPLATFVRRLG--PQWR--LVQRGDPAAFRALVAQLVC 57
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:
RTGGATTLSLRGLGVLTIVETDTLPVGIGIKVPVLLEGDSEKFRSFAELVLC 60
OARPPAAPSRQVSCLVELVARVOLRLCERGAKNVLAFLGFALLDGARGGPPEPTT 117
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:
3TKPLSPSVSLQSSTQEVARVIORICEKKGNKLAFGYGLVD-EKNLSNIRLTP 119
SYLENVTDALRGSGAWGLRRVGDVVHLHILALCALFVLAVAPSAYCVCGPLY- 176
NYFPNPPTTTISILWELLITRVGDVMYMLEQCISIFVPPPCCYQITGOPIYT 179
-----OLGAQTAR-----PPPHASGRPRRLGCERAMNHVSVE 209
DVLFPSOSFTOSTNLRYIKENVFLHRKYLYKPXHSMTSM-----LTHRNKSP 234
?LGHPAGARRRCGSARS|- - - - PLPKRPRRGAPE-----PERTPVQG 254
JRSKTSMATTVTEIHSKRKCLKNDICVIPDKKRDLDDKDXTDFHDLPMSCSVYL 294
IPGR-----TRG-PSDRGFCVSPARPABEATSLEGALSGTRH----- 294
?PTNTVOVTGLITSYGKTKTFQCCKPVSCBOKKTAFFYSVAGDCNLSLKONVKLI 354
VGRQHAGAPPSTSRRPDWDTCPPPYAEATHKFY-LSSGDKEQLRPSFLSSLRPS 353
V-----PTAQSR-----LSFSNFIDFGRTLISISKKSFEFILNSLDST 401
ARLVETIFLGS-----RWMPCTPRRLPRLPORYQMWRPLFLLEIGHACQP 405
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:
OKLVETIELSNLABQNFDQPCROENCRY--KLPKRYWKMKPFHQELIQHKXPFY 459
KTHCPRLAAVTPAAGVCAREPQGSVAPEED-----TDPRRLVOLLROHSS 457


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523 523
23 AA; 56555 MW; 8FDE562DDECC93DA CRC64;
    37.0%; Score 2207.5; DB 4; Length 523;
    78.7%; Pred. No. 4.7e-162;
    3; Mismatches 56; Indels 59; Gaps 6;
    Conservative
APRCRAVRSLLRSHYREVLPLATVRLRGQWRLVORGDPAPAFRALVAOCLVCPW 60
APRCRAVRSLLRSHYREVLPLATVRLRGQWRLVORGDPAPAFRALVAOCLVCPW 60
PPPAAPSFROVSCCLKEIVARVQLRCLCERGANVLAFAFALLDGGARGGPPPAFTTSVR 120
PPPAAPSFROVSCCLKEIVARVQLRCLCERGANVLAFAFALLDGGARGGPPPAFTTSVR 120
PPPAAPSFROVSCCLKEIVARVQLRCLCERGANVLAFAFALLDGGARGGPPPAFTTSVR 120
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PNTVTDALRGSGAWGLLLRRVGGDDVLVHLLARCALFVLVAPSCAYQVCGPPLYLQGA 180
ARPPPHASGRRRLGGERANVHSREAGVPLGLPAPGARRRGGSASRLPLPKRPR 240
ARPPPHASGRRRLGGERANVHSREAGVPLGLPAPGARRRGGSASRLPLPKRPR 240
ARPPPHASGRRRLGGERANVHSREAGVPLGLPAPGARRRGGSASRLPLPKRPR 240
PEPERTVGQSGWAHPGRTGPGSDRGFCVVSPPAPAEATSLGALSGLTRHSPSVG 300
PEPERTVGQSGWAHPGRTGPGSDRGFCVVSPPAPAEATSLGALSGLTRHSPSVG 300
PEPERTVGQSGWAHPGRTGPGSDRGFCVVSPPAPAEATSLGALSGLTRHSPSVG 300
HAGPPSTSRPPMDTCPPIVYATKHLFVSSGDKQLRPSFLSSLRPSLTGARRL 360
HAGPPSTSRPPMDTCPPIVYATKHLFVSSGDKQLRPSFLSSLRPSLTGARRL 360
HAGPPSTSRPPMDTCPPIVYATKHLFVSSGDKQLRPSFLSSLRPSLTGARRL 360
IFLGSREPMWGTTPRLPLRPLRYWOMEPLFELLLGNHAQCPYGVLLKTHCPPLAAVT 420
IFLGSREPMWGTTPRLPLRPLRYWOMEPLFELLLGNHAQCPYGVLLKTHCPPLAAVT 420
IFLGSREPMWGTTPRLPLRPLRYWOMEPLFELLLGNHAQCPYGVLLKTHCPPLAAVT 420
GVCAREKPGQSGAAPEEEDTPRLVQLLRQHSPPQVYGVRACLRLRVPPGLW-- 478
--CELRSFQPPVSPV--GRSPRAL-----W-----RPPRRRTTPVWCS 450
-----GSRHNERFLRNTKFKISLGKHAQSLQELTWK 511
STAPLAGVRLRAGLPAPAGAPRPLGLQARRRFLRNTKFKISLGKHAQSLQELTWK 510
RDCAWLRSP 524
RDCAWLRSP 523
PRELIMINARY; PRT; 575 AA.
(TREMBLrel. 15, Created)
(TREMBLrel. 15, Last sequence update)
(TREMBLrel. 25, Last annotation update)
atalytic subunit (Fragment).
icus (Rat).
atazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
0116;
N.A.
S., Xu X., Yu H.;
ase catalytic subunit, rTERT.";
AR-2000) to the EMBL/GenBank/DBJ databases.
18; AAF62177.1; -.
34; C:nucleus; IEA.
77; F:DNA binding; IEA.
23; F:RNA binding; IEA.
54; F:RNA-directed DNA polymerase activity; IEA.
21; F:telomeric template RNA reverse transcriptas. .; IEA.
40; F:telomerase activity; IEA.
78; P:RNA dependent DNA replication; IEA.

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DR InterPro; IPR000477; RVTse.
DR InterPro; IPR003545; Telomerase_RT.
DR Pfam; PF00078; rvt; 1.
DR PRINTS; PR01365; TELOMERASERT.
KW RNA-directed DNA polymerase; Transferase.
FT NON_TER 1
SQ SEQUENCE 575 AA; 65672 MW; F80C81BD7F6A91A3 CRC64;

Query Match 33.8%; Score 2016; DB 11; Length 575;
Best Local Similarity 67.6%; Pred. No. 3.5e-147;
Matches 391; Conservative 71; Mismatches 110; Indels 6;

QY 558 RSFFYTTTFOKRLFFYRKSVMSKLSQISIGIRQHLKRVOLRELSAEVRQHREA
DB 1 RSFFYTTTFOKRLFFYRKSVMSKLSQISIGIRQHLKRVOLRELSAEVRQHREA
QY 618 TSLRLPIPKDGLRPIVNDYVVGARTPREKRAELTSRVKALFSLVANYERARR
DB 61 ICLRLPIPKDGLRPIVNDYVVGARTPREKRAELTSRVKALFSLVANYERARR
QY 678 ASYLGDDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASI
DB 121 SSVLGWMDIYRTWRAFLVLRALDQTPRMVYFKADVTGAYDAIPQGLVEVVANM
QY 737 NTYCVRYAVVOKAAGHVRAKAFKSHVSTLTDLQPYMROFVAHLQET--SPLRDA
DB 181 STYCIQYAVVRDSQGVHKSFRQVTTLSDLQPYMGQFLKHLQSDSALRNS
QY 795 SSSLNEASSGLFDVFLRFMCHAVRIRGKSYVQCQIPQGSITLSTLCSLCYGDGM
DB 241 SISMNESSSLDFDLHFLRHSVVKIGDRCYTCCQIPQGSITLSTLCSLCYGDGM
QY 855 AGIRDDGLLRLLVDVDFLLVTPHLLTHAKTFLRLVRGVPYGCYVNLKRTVVPFV
DB 301 AEVQRDGLLRVDFDVLVTPHLLTHAKTFLRLVRGVPYGCYVNLKRTVVPFV
QY 915 GGTAFVQMPAHGLFPWCGLLLDTRILEVQSDYSSVARTSIRASLIPNRFKAGRN
DB 361 GAAAPYQLPAHCLFPWCGLLLDTRILEVQSDYSSVARTSIRASLIPNRFKAGRN
QY 975 FGVLRLKCHSLFLDQVNSLQVTCNIVYKILLQAVRHACVQLQLPFHQQVKNP
DB 421 LSVLRKCHGLFLDQVNSLQVTCNIVYKILLQAVRHACVQLQLPFHQQVKNP
QY 1035 VTSATSLCYSLKAKNAGSLGAKGAGPLPSEAVQMLCHQAFLLKLRHRTVY
DB 481 IISQASCCYAILKVNKPGMTLKSGS---PPEAAHMLCYQAFLLKLAHSVY
QY 1095 SLRTAQTLRSLKPGTTLTALEAANPALPSPDKTILD 1132
DB 538 PLRTAQKLLCRKLPRATMTILKAAADPALSTDFQTILD 575

RESULT 9
Q9R266 PRELIMINARY; PRT; 514 AA.
AC Q9R266;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Telomerase reverse transcriptase (Fragment).
GN TERT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=99144726; PubMed=1002128;
RA Greenberg R.A., O'Hagan R.C., Deng H., Xiao Q., Hann S.R., Adams
RA Lichtsteiner S., Chin L., Morin G.B., Depinho R.A.;
RT "Telomerase reverse transcriptase gene is a direct target of c-M;
RT is not functionally equivalent in cellular transformation.";

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1219-1226(1999).
 349; AAD2465.1; --
 364; F:RNA-directed DNA polymerase activity; IEA.
 1 DNA polymerase.
 514 514
 514 AA; 58382 MW; 30965997769BBFD CRC64;
 23.0%; Score 1373; DB 11; Length 514;
 ilarity 56.1%; Pred. No. 1.6e-97;
 Conservative 50; Mismatches 142; Indels 46; Gaps 10;
 IAPRCRAVSLRSHYREVLPLATFVRRLLPGQWRLVQSGDPAFAFALVAQCLVCPW 60
 IAPRCFAVSLRSHYREVLPLATFVRRLLPGQWRLVQSGDPAFAFALVAQCLVCPW 60
 IAPPAFSPFQVSLKELVARVLQRCERGAKNVLAFFGALLDARGGPPPEAFTTSVR 120
 IAPPADLSFQVSSKELVARVVRQRCERNVLAFFGALLDARGGPPPEAFTTSVR 120
 IAPVTDALRGSGAWGLLRRVGGDDVLAHLLARCALFVLVAPSCAYQVCGPPLYLGA 180
 IAPVTLETURVSGAWMLLRSRVGGDDVLAHLLARCALFVLVAPSCAYQVCGPPLYLGA 180
 IAPPPHAS-GPRRLG-----CERAWNSVREAGVPLGLPAPCARRGGSASRS 231
 IAPWSVASVYRTPRVGRNFTNLRFLOQIKSSSRQAPKPLALPSRGTGKHLSTSTS 240
 IAPRRGAAPPERTFVQGGWAHPGRTRGPDGFCVVSAP-----PAREATSLE 286
 IAKARCYVPVVEEGP-----HRQVLPFGKSW-VPSAPSPVPTAEKDLSSK 292
 IAGTRHSPVSGRQHAGPPSTSRPRPMDTFCPPVYATKHYLYSSGD-KEQLRPSF 345
 IADLSL-GSVCKKPKSSTLSPPRQNAFQLRP-FIETRHLYSRGDGQRLNPSF 350
 IALRSLTGARLVETIFLGSPPMPTGTRPLRPLQRYWQMRPLFELHGNHACPY 405
 IALQNLATGARLVETIFLGSPPMPTGTRPLRPLQRYWQMRPLFELHGNHACPY 410
 IALHCPPLAA---VTPAGVCAKPKPGSVAAPBEEDTPRRLVQLLRQHSSPMQVY 462
 IALRSHCFRTANQVTDAL-----NTSPHMLDLRLHSSPMQVY 452
 IALRRLVPPGLWGSRRNERFELNTKFKFISLGHAKLSLOELTWKMSVRDCAWLRR 522
 IALRCKVVSASLWGRNERFFKRLKFKFISLGHAKLSLOELTWKMSVRDCAWLRR 512
 524
 514
 PRELIMINARY; PRT; 1123 AA.
 (TrEMBLrel. 13, Created)
 (TrEMBLrel. 13, Last sequence update)
 (TrEMBLrel. 25, Last annotation update)
 reverse transcriptase catalytic subunit.
 :haliana (Mouse-ear cross).
 iridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 a; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 Brassicales; Brassicaceae; Arabidopsis.
 702;
 4 N.A.
 berg erecta;
 9564; PubMed-10611295;
 S., Riha K., Gao F., Ren S., McKnight T.D., Shippen D.E.;
 of the telomerase catalytic subunit gene from Arabidopsis
 telomerase and leads to a slow loss of telomeric DNA."

Proc. Natl. Acad. Sci. U.S.A. 96:14813-14818(1999).
 EMBL; AF172097; AAD54276.1; --
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
 DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
 DR GO; GO:0003721; F:telomeric template RNA reverse transcriptase.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006278; F:RNA dependent DNA replication; IEA.
 DR InterPro; IPR000477; RVTse.
 DR InterPro; IPR000215; Serpin.
 DR InterPro; IPR003545; Telomerase_RT.
 DR Pfam; PF00078; tvt; 1.
 DR PRINTS; PR01365; TELOMERASERT.
 DR PROSITE; PS00284; SERPIN; 1.
 DR RNA-directed DNA polymerase; Transferase.
 KW SEQUENCE 1123 AA; 130551 MW; 44F248295817B7F6 CRC64;
 Query Match 12.2%; Score 724.5; DB 10; Length 1123;
 Best Local Similarity 23.9%; Pred. No. 7.1e-47;
 Matches 294; Conservative 192; Mismatches 506; Indels 237;
 QY 1 MPAPRCRAVSLRSHYREVLPLATFV-----RRLGPGQWR-----
 DB 1 MPAPRCRAVSLRSHYREVLPLATFV-----RRLGPGQWR-----
 QY 39 VQGDPAFAFALVAQCLVCPWDAAPPPAPSPQVSLKELVARVLQRL---CI
 DB 61 LRSDDPTFHYKELHRCFV-VLHEQTPLPLDFSPSWMQREIVERIEMQSGCI
 QY 96 VLAFGPALLDARGGPPPEAFTTSVRSVLPNTVTDALRGSGAWGLLRRVGGDDVLA
 DB 118 VICARYDYQS-----SPILELLT-SSSWEFLKRVGHDVM
 QY 156 CALFVLVAPSCAYQVCGPPLYLGAAT-----QARPPPHASGPRRLGCEAWN
 DB 160 TSIFPLGLKHKHQVSGPPLCIKHKRTLSVHENKRRKDDNVQPTKQWLSSAVI
 QY 210 AGVPLGLPAPG-----ARRGGSASRLPLPKRPRGA-----APEPRTFVC
 DB 220 DSATI-TPVIGEDVDQHKRKKTKRSRIYLKRRKQKRVNFKKVDGNAPCITP--
 QY 258 HPGRTGPSDRGFCVVSAPPAPEATSLGALSGTRHSHPSVGRHAGPPTSR
 DB 272 ---STNGKYSTG-----NDENNLHIGINGSLTDFVKQAKQ-----
 QY 318 DTPCPVYATKHYLYS-SGDKEQLRPSFLLSLRPSLTGARLVETIFLGSRPW
 DB 304 -----VKRNKNFKPLSETYSVIPPNHLLKTLRNCSDSKLLMNHIFGEVNVK
 QY 377 RLPLRPQ-----RYQWRPLFELHGNHACPYGVLLKTHCP-----LRAAV
 DB 357 HGKGNCPGSGICLYHSLKSLKLNLIKTKTSSHLKMLLDKHCPLVLLQEDALSGT
 QY 425 VCAREK-----POGSVAA-----PEEDTDPRRLVQLLRQHSSPMQVYFVACLR
 DB 417 --RQKADKLPHGSSSSQTKPKCPSVEERKL-----YCTNDQVVSFWIACRY
 QY 477 LMGSRHNERFLRNTKFKFISLGHAKLSLOELTWKMSVRDCAWLRRSPGVCVPA
 DB 469 LLGTTHQMRVLKNIAMFVSRRENEKCTVQFLHKVKPSDFFPFARKE--LCMV.
 QY 537 REE-----ILAFELHWSVYVVELLRSFYVTTTFOKNRFFFKYKSVWSK
 DB 527 QSESTRSQMLCTKWIEMFLFLEIVKLVHFNFYATESQGRNLNYYVYKRGRWER
 QY 589 IQHLLKRVQLRELSEAVRQHRERAPALLTSRLREIPEKPDGLRPVNMDDVVGAR
 DB 587 ISKALDGVVLDAAESRRK-----LSKRFPLKANGVRMVLID-----
 QY 649 KRAEELTSRVKALFSLVNYERARRPGLLGASVIGLDDIHRAWRTFVLVRVADPP

QSL-----RDTHAVLKDIQKEPDVLGSSVDFHDDFYRNLCVPLIHLRSQSSELPPLY 696
 YDVTGAYDTIPQDRLETVIASIIPONTYCVRRYAVVQAAHGH-----VRKAFKS 761
 ADVFAFDSDQGLLHVIFQLKDE--YILNRCRLVCCGKRSNWVKILVSSDKNS 744
 ITLTDLOPMQRFVAVHLOSTPLRDVAVIEQSSLINEASSGLDFVFLRMCHHAVIR 821
 IRTSTVPYNA-----LQ-----SIVVDKGENHRVRKKDLVMWIGNLKNMLQLD 792
 YVQCGIIPQGSILTLCLSLCVGMENKLFAGI-----RRDGL-----862
 YVQIAGIQGHRSLSCFYGHLERTLIPFLEEASKVSSKECSREELIIPTS 852
 LRLVDLFLVTHLTHAKFTLRTLVRGVPEYGCVVNLKRTVNFPEVE-----912
 LRFIDYLFVSTSRDQASSFVHLKHGKDYNCFMNETKFCINFEDKEHRCSNRM 912
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 DNGVPFVR-----WTGLINSRTFEVDYTRYLSGHISSTFSVAMQKPVRL 964
 LFGVLRUKCHSLFLDLQVNSLQTVCTNIYKILLQAVRFHACVLQLPQOQVWK-NP 1029
 LCYELVPKCHPILFDSNINSGEIVRLNIYQIFLLAANKFHCYVYEV---SRFWKLHP 1021
 LRVSTASLCSYLKAKNAGMSLAK-GAAGPLPSEAVQWLCHQAFLLKLTRHRT 1088
 FKFTISVRYMFRILNRRVRRINTGSSRPVLKLYKEEVIWLGDAVIQVLKKNRS 1081
 LLSLRTA-----QTOLSRKLPGTT 1111
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PRELIMINARY; PRT; 1123 AA.

(TREMBLrel. 13, Created)
 (TREMBLrel. 13, Last sequence update)
 (TREMBLrel. 25, Last annotation update)
 E19.190.
 Thaliana (Mouse-ear cress).
 iridiplanaceae; Streptophyta; Embryophyta; Tracheophyta;
 a; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 Brassicales; Brassicaceae; Arabidopsis.
 702;

N.A.
 Columbia;
 2974; PubMed=10471830;
 Iu H., Tamura K., Takahashi H.;
 loning and characterization of ActERT, a telomerase
 scriptase homolog in Arabidopsis thaliana.";
 57:465-469 (1999).

N.A.
 amura Y., Kaneko T., Kato T., Asamizu E., Kotani H.,
 swes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
 JG-2000) to the EMBL/GenBank/DBJ databases.

N.A.
 is sequencing project;
 UG-2000) to the EMBL/GenBank/DBJ databases.
 54; AAD54777.1; -
 47; CAC01849.1; -
 T51517.

34; C:nucleus; IEA.
 77; F:DNA binding; IEA.
 23; F:RNA binding; IEA.
 54; F:RNA-directed DNA polymerase activity; IEA.

DR GO:0004867; F:serine protease inhibitor activity; IEA.
 DR GO:0003721; F:telomeric template RNA reverse transcriptase.
 DR GO:0016740; F:transferase activity; IEA.
 DR GO:0006278; P:RNA dependent DNA replication; IEA.
 DR InterPro; IPR000477; RVise.
 DR InterPro; IPR000215; Serpin.
 DR InterPro; IPR003545; Telomerase_RT.
 DR Pfam; PF00078; rvt; 1.
 DR PROSITE; PRO1365; TELOMERASERT.
 DR PROSITE; PS00284; SERPIN; 1.
 DR RNA-directed DNA polymerase; Transferase.
 KW RNA-directed DNA polymerase; Transferase.
 SQ SEQUENCE 1123 AA; 130579 MW; 5645B8295817B7F6 CRC64;

Query Match 12.2%; Score 724.5; DB 10; Length 1123;
 Best Local Similarity 23.8%; Pred. No. 7.1e-47;
 Matches 294; Conservative 199; Mismatches 511; Indels 233;

QY 1 MPAPRCRAVRSLLRSHYRVLPLATFV-----RRLGQGMW-----
 DB 1 MPRKPRHVRPEILLWLFGRNARNLDAIVLIPNRNIQPCRCRGQGLCGSSI
 QY 39 VORGDDPAAPALVAQCILVCVPMDARPPAPSPFQVSCLELYAVLQRL---CE
 DB 61 LRDDPIHRYKLLHRCFV-VLHEQTPELDLDFSPTSWMSQREIVERIEMQSGCI
 QY 96 VLAFGFALLDARGGPPPEAFTTSVRSYLPNTVTDALRGSGAMGLLLRRVGDVLA
 DB 118 VICARYDKYDOS-----SPILELLT-SSSWEFLKRVGHVWV
 QY 156 CALFVLVARSQVQVCGPPLYLQGAAT-----QARPPPHASGPRRLRGCEAWK
 DB 160 TSIFLPLGKGHQVSGPPLCIKHRTLSVHNKRKRDNDVQPTKQWLLSSAVL
 QY 210 AGVPLGLPAPG---ARRGGSASRSILPLKPRRCA-----APEPERTVPG
 DB 220 DSATI-TPVIGEDVDQHKETTKRSRIYLRKRKORKVNFKKVDCNAPCITP--
 QY 258 HPGTRGSDRGFCVVSPPAPAEATSLGALSSTGRSHSPSVGRQHHAGPSTSR
 DB 272 ---STNGKYSTG-----NDENMLHIGINGSLTDFVKQAKQ-----
 QY 318 DTPCPPVYAEATHFLYS-SGDKEQLRPPSLSLRPSLTGARLLVETIFLGRSPW
 DB 304 -----VKRNKNFKGLSETYSVIPPNHILKTLRPNCSKILMNHIFGEVNVW
 QY 377 RLRLPLPQ---RYQMRYPLFLELGNHAQCPYGVLLKTHCP-----LRAAV
 DB 357 HGKGNCPGSGICLYHSLKSLKLNLIKTKSSHLMULDHCHPCVLLQEDALKSGT
 QY 425 VCAREK---PQGSVAA-----PEEDTDPRRLVQLLRQHSPPWQVYGFVRACLRR
 DB 417 --RRQKADKLPHGSSSSQTKPKCPSVEERKL-----YCTNDQVVSFWAICRY
 QY 477 LWSRNERFRINTKFTSLGKHAKLSLQELTWMVSVDCAWLRSPGVGCVPA
 DB 469 LIGTTHOMEVLRKNTAFVSRRENEKCTVQFLHKVKSDFPFARKE--LCCMV
 QY 537 REE-----ILAKFLHLMVSVVVELRSFFYTETTFQKNLFFFYKSVWSK
 DB 527 QSESTRSTQOMCTKWIWSLFLIYVKLVHFNFYATESQGRNIYYIKRWSER
 QY 589 IFQHLKRVQLRELSEAEVRQHREARPALTSRLRFPKPDGLRPIVNMDDYVVGAR
 DB 587 ISKALDGYVLVDDAEASSRKK-----LSKRFPLKANGVRWVLD-----
 QY 649 KEAERLTSEVKALFSLVNYERARRGLIGASVLGLDDTHRAWRTFVLVRADPP
 DB 631 SRSQSL-----RDTHAVLKDIQLKEPDVLGSSVDFHDDFYRNLCVPLIHLRSQSSEI
 QY 708 FVKVDVTGAYDTIPQDRLETVIASIIPONTYCVRRYAVVQAAHGH-----VRI
 DB 687 FVADVFKAFSDVQGLLHVIFQSLKDE--YILNRCRLVCCGKRSNWVKILVSI

TLTDLQPMQVFAHQLQTSPLRDAVWIEQSSLSNEASSGLDFVFLRFMCHAVRIR 821
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 YVQIAGIPQGRHLSLLCCFYGHLETLIYFFLEASKOVSSEKCSREBELIPTS 852
 LRLVDDFLVTPHLETHAKTFLRTLVRGVPEYGVVNNKRTVNNPVEDE----- 912
 LRFIDYLVFVTSRDQASSFVHRLKHGKDYNCNPNKTCINFEDEKHEHRCSSNM 912
 LGGTAIVQMPAHGLFPFGCLLDTTLEQSDYSYARTSIRASLTFRNGFKAGNM 970
 DNGVFFVR-----WTGLLINSKTFEVQVDYTRYLSGHISSTFSVAWQNKPVRL 964
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 LCYFLVPKCHPILFDSNINSGEIVRLNIYQIFLLAAMKPHYCYVEV---SRFWKLHP 1021
 LRVISDTASLCYSILKAKNAGMSLCAK-GAAGPLPSEBAVOMLCHOAFLLKLTTRHVT 1088
 FKETISVRYMFRLINRVRINTGSSFRPVLYKLYKEVIMWGLDAVIQVLKKNR 1081
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 LLIYLSALSLSLQSLSELRYATDRSNSSL 1118

PRELIMINARY; PRT; 1259 AA.

(TrEMBLrel. 17, Created)
 (TrEMBLrel. 17, Last sequence update)
 (TrEMBLrel. 25, Last annotation update)
 everse transcriptase.

(rice).
 iridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 a; Magnoliophyta; Liliopsida; Poales; Poaceae;
 e; Oryzeae; Oryza.
 530;

M N.A.
 amura K., Takahashi H.;
 loning and characterization of OstERT, a telomerase
 scriptase homolog in Oryza sativa.";
 UL-2000) to the EMBL/GenBank/DBJ databases.
 16; AAK35007.1; -
 113; -

34; C:nucleus; IEA.
 40; C:ribosome; IEA.
 77; F:DNA binding; IEA.
 23; F:RNA binding; IEA.
 54; F:RNA-directed DNA polymerase activity; IEA.
 35; F:structural constituent of ribosome; IEA.
 21; F:telomeric template RNA reverse transcriptase. .; IEA.
 40; F:transferase activity; IEA.
 12; P:protein biosynthesis; IEA.
 78; P:RNA dependent DNA replication; IEA.
 R001209; Ribosomal_S14.
 R000477; RVTse.
 R003545; Telomerase_RT.
 8; rvt; 1.
 365; TELOMERASERT.
 0527; RIBOSOMAL_S14; 1.
 DNA polymerase; Transferase.
 259 AA; 143710 MW; 158041789F2D5CAD CRC64;

11.5%; Score 688; DB 10; Length 1259;
 larity 23.9%; Pred. No. 5.5e-44;
 Conservative 175; Mismatches 486; Indels 312; Gaps 45;

QY 36 W-RLVQGDPAAPRALVAQCLVCVPMW---ARPPAAPSPROVSCLEKELVARVL
 DB 66 WEHLRDGDPIAYRRLITRAVCAIAADLAPPPRYTPGNSGHSQARLVREMMI
 QY 90 -ERGAKNVLAFGFALLDARGGPPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRI
 DB 126 QSHGTKNVLCNG--LHEGGQ-----SICISDLVSSSSWSLILHI
 QY 149 LVHLLARCALFVLVAPSCAYQVCGPPL-----YOLGAATOARPPPHASGPRRLC
 DB 168 MCYLLRCTSIFLFPVKKNDYFQVSGVPLNVLNRP1FASVARKHQPOTTAKCH
 QY 204 N-----HSVREAGVPLGLPAP-----GARREGGS--ASRSLI
 DB 227 KSNAMENLSICHDSNNSGVNSFSSTCKIVTQOSETCGSIIRRAESKDPSEGC
 QY 239 RRGAAPE-----PERTVPGGQSWAHGR-----
 DB 287 SDGRSGECNCYTHNTRKRLYSWQRRSKKQVCSVDSESAEWSKLNGSNFNE
 QY 267 -----DRGFCV-----VSPAPAEATS-----LEGALSCTRHSHPV--
 DB 347 NLAGKMDQAQSVELTVDNSTLARSNDSDSSEIKVINATILSEKSPCSVFDIRC
 QY 303 -HHAGPSTSRPPRPMDTPCPVVAETKHELYS-----SGDKBQLRPSFLI
 DB 407 CHY-----SLSEVOYQSTCPQVGPSSYHLNCSICFNCCIISNAKSLDLSLI
 QY 353 SLTGARRLVETIF-----LGRSP-----
 DB 459 GIFYNRRTTVSVPHCKHILSKRKPDAISLVKHI FGINSCCASILKYNCHESTIF
 QY 371 --WMPGTTPRLPRLPORYQWMPRELFLLEGNHAQCPYVLLKTHCPILRAAVTP--
 DB 519 CCWLPKSIKNLIR-----NSKRCQYKKLFLKHCSYKCKVAPDV
 QY 427 AREKPOGSVAAPEEEDTPRLVOLLRQHSSPMQVYGFVRACLRLVPPGLWGSF
 DB 562 KAHYFPGGKAAYD-----RSFSRLIAYSTHOQVASFVWAVLKRIVPKELLGNF
 QY 487 FLRTTKKIFSLGHAKHAKLSLQELTMKMSVRDCAWLRR-----SPGVGCV
 DB 616 LRTNIWKFILKRRFETFQLSDCIGDLKVSHYSWLSNIEFSNCFCSALIGQTGSS
 QY 535 RUEEEILAKFLHLMGMYVVELLRSPFYVTTFTFQKRLFPYKKSWSKLQSTGI
 DB 676 QROKNILHCMISWLFSDIVIPVVRTYFYTERESKRYDYFYPKSVMRDLTSNAI
 QY 595 RVQLRELSAEVROHREARPALITSLRFLPKDPGLRPIVNMDDYVVGARTFREK
 DB 735 KKNFRIL-RGEPR--KAVZHLNCSVRFLPKAKDNRLPLVDL-----
 QY 655 TGRVKALFVNLVYERARRPGLLGASVGLDDTHRAWRTFVLVRVRAQ-DPPPELYF
 DB 779 DANLANKCHLIMKKLRDEKDEMPGSSVFDVNNVHQLNSQFISSKRSQIMKKLVYI
 QY 714 TGAYDTIPODRLTEVTASIIKQNTVCYRPAVYVQAAHGHVRKAFKSHVS-----
 DB 839 SKAFDCVSHDMVLKMDIDDAFK-CDEYTVRKCSKVICNRSKNSLYRFDNSNAGNG
 QY 769 LQPYMRQFVAHLQETSPLRDVAVVIEQSSLSNEASSGLDFVFLRFMCHH-----
 DB 898 LS-----IQLSS--GGGIFVDQ-----GTICRIKQEPHLLLYEQIK
 QY 820 IRGKSYVQCGIPQGSILSTLCSLCYGDWENKLPAGIRRDG-----
 DB 938 IQQKYVLLQGVGAQGSKLSPNLCSLYGYHLENSVLSKFLHDSKLNAGEAFSEPEY
 QY 867 VDDFLVTPHLETHAKTFLRTLVRGVPEYGVVNNKRTVNNP-----PVEDSALG
 DB 998 IDDFIFISFLEHAQKFLNRMRGFFVFCYVNCYNDKSGYGFNCAGNSEPSSNLYR

'AHGLFPACGILLDTRTLEVCQSDYSSYARTSTRASLTNRGFKAGNRMRKLFVGLRL 980
--SWPWSGLINCETTELIEIADYTRYLDITITITVV-KMHSSTKYTHSKLCHTMPR 1111

(SLFDLOVNSIQTVCTNIYKILLQAYRFHACVLQLPFHQOVWKNPTFFLRVISDTA 1040
IPFYDSNINSPTGRVNIYQAFLLCAMKFH-CYIRSVDANVS-K-LELLQVIKRTF 1168

'YSILKAKVAGNSLAGKAGAGPLPEAVQWLCHQAF--LLKLTRHRVTYVPVLGSLRT 1098
:::
HSLIVRRMQDVEL-----HYNVRPVLKRREKTILWLGTLTAIRV 1210

'QLSRKLPCTLTALE 1116
:
'KQSYKDWMLTLTAE 1228

PRELIMINARY; PRT; 1261 AA.

(TREMBLrel. 22, Created)
(TREMBLrel. 22, last sequence update)
(TREMBLrel. 25, last annotation update).
reverse transcriptase.

((japonica cultivar-group).
iridiplantae; Streptophyta; Embryophyta; Tracheophyta;
a; Magnoliophyta; Liliopsida; Poales; Poaceae;
e; Oryzeae; Oryza.
.9947;

M N A.
lipponbare;
6152; PubMed=12100484;
ska K., Schnippenkoetter W., Killian A.;
characterization of rice (*Oryza sativa* L) telomerase
iscriptase, which reveals complex splicing patterns.";
75-86(2002).
.53; AAM21641.1; -.
XWO; "-
.34; C:nucleus; IEA.
.40; C:ribosome; IEA.
.77; F:DNA binding; IEA.
.23; F:RNA binding; IEA.
.64; F:RNA-directed DNA polymerase activity; IEA.
.35; F:structural constituent of ribosome; IEA.
.21; F:telomeric template RNA reverse transcripts. . ; IEA.
.40; F:transferase activity; IEA.
.12; F:protein biosynthesis; IEA.
.78; F:RNA dependent DNA replication; IEA.
R001209; Ribosomal_S14.
R000477; RVtse.
R003545; Telomerase_RT.
8; rvt; 1.
.365; TELOMERASERT
.0527; RIBOSOMAL_S14; 1.
DNA polymerase; Transferrase.
261 AA; 143715 MW; 353153DC8B7D5CB CRC64;

11.0%; Score 654.5; DB 10; Length 1261;
larity 23.6%; Pred. No. 2.2e-41;
Conservative 173; Mismatches 500; Indels 337; Gaps 48;

'LSLRSHREVLPATFVR-----LGPQG-RUVQRGDPAAFRALYAQCLVCVPWD 61
||| :
'FSLSPRHCSPPCAPCRGRVASGCLACRWHEHLRDGDPVAVRRLITRAVCAIAAD 92

ARPPAPASPFRQVSCLELVARVLQRLC---ERGAKNVLAFGALLDGARGGPEAF 115
||| ||| | :
'APPPRTPYPGNSGHGSQARLVREMMSIVAQOSHGTKNVLCNG--LHEGGQ----- 143

'VSYLPTNTVDALRGSGAWGLLLRVGDDVLWHLLARCALFLVAPSCAQVCGPPPL 175

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NIYQAFLLCAMKFH-CWIRSVSDANVK--LELQVTKRTPRYMHSILVIRMQDVEL 1188
GAAGLPSEAVQWLCHQAF--LLKLTRHRVTYVPLLGLSLTAQTQLGRKLPGTTLTA 1114
      :|||:      :|:      :|:      :|:      :|:      :|:
-----HYNVRPVLKLRKETIWLGLTAIVRVLQOKQSRYKDXMLTLT 1228
1116
1230

PRELIMINARY;      PRT; 1032 AA.

(TREMBLrel. 25, Created)
(TREMBLrel. 25, Last sequence update)
(TREMBLrel. 25, Last annotation update)
everse transcriptase.

ssus.
lveolata; Ciliophora; Spirotrichea; Hypotrichia;
uplotidae; Moneuplotes.
936;

M N.A.
Z., Wang L., Shrode T., Bednenko J., Hurley L.A.,
;
ally programmed gene elimination in Euplotes crassus
a switch in the telomerase catalytic subunit.";
003).
43; AAP42278.1; -.
DNA polymerase.
032 AA; 123265 MW; C44E30B6D6D37953 CRC64;

8.08; Score 478; DB 5; Length 1032;
larity 24.8%; Pred.No.7.3e-28;
Conservative 110; Mismatches 276; Indels 76; Gaps 19;

RFLRNTKKFTSLGHAKLSLQELTWKMSVDRDCAWLRSSPGVCPAAEHLREE---539
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SPQSKIKKYVLGNKHELHKNLLGLKLDIKSIKWL-----GFTSKQNYHYFDKENRF 434
KFLHLMMSVYVVELLRFFYVTTTFQKNRLFFYKRSVWSKLOSIGIRQHLKRVQLR 599
RILRWIPEDVVVSLIRCFYVTEQOKSYSETYYVYKNIWDIVMKYSIAD--LNRETL 493
SEAEVROHREARPAALLTSRLRFPKPGCLRPVNMVTVGARTFR-----EKRAER 653
KEDMVQWKNELRFA--EGKLRLPKKTTPRIM-----TFNKIVDPEGKTSK 542
RVKALFVLNVERRR--PGLLGASVLGLDDIHRAWRTFLVRAQDPPPELYFVK 710
      |||:      |||:      |||:      |||:      |||:      |||:
NTKLSYSHLMKTLKRNMFDPGFVNFDDVNRKYEEFVLKWRQVD--RPKYFVT 601
TGAYDTIPDRLTEVIAS-----IIPQNTYCVRYAVVQKAAHGHRV 756
      |||:      |||:      |||:      |||:      |||:      |||:
EKCVDSVDREKLSQFLGTTQLLSPNFQIIVQVILKRNNVIVDSQNFKKKMDYFR 661
KSHVSTLTDLPYWRQFVAHLOETSPURDAVITQSSLSNEASGLFDVFLRPMCHH 816
      |||:      |||:      |||:      |||:      |||:      |||:
QK-IALEGDQYPSLFNVLENDQNELNAKTLTVENQKRDYPYKKKALLDPVIKICRH 720
IRGSYYQCOGIPGGSITLLCLSCYGDMEKNLKFAGIRRDG-----LILLRV 867
      |||:      |||:      |||:      |||:      |||:      |||:
FNRKYVQTGIPGCLCVSSILSSFYASLEENALGYLRKESMDANDPNTLLMLRT 780
LLVTPHLTHAKTFLRTLVRGVPYCGCVNLRKTVNPPVEDEALG--GTAFV--QMP 923
      |||:      |||:      |||:      |||:      |||:      |||:
LLTTIKENALLFIEKLINVSRQNKFKFNKKLQTNFPLDPSKLNKYGHASVEDQNI 840
LFPWCGLLLTDTRELVOSDYSSYARTSIRASLTFN--RGFKAGNRMRKFLGVLRKLC 982
      |||:      |||:      |||:      |||:      |||:      |||:

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Db      841 AHDIYIDWIGISDMSTALMPNI--NLRRKGILCTLNNMNQTKCASMWLKRKL--
Qy      983 HSLFLDLQVNSLTQVCTN-----LYKILLQAVRFHACVQLQLPFPHQVWKNP
Db      892 KSLFMNITRYFRKTYITREFSNKTLNKLYTAGAYKYMCCIEYKDHFT--NTI
Qy      1036 ISDTASLCYSILKA 1049
Db      950 DKIIICAIIVSVTRA 963

RESULT 15
Q8MUB3
ID      Q8MUB3      PRELIMINARY;      PRT; 1032 AA.
AC      Q8MUB3;
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Telomerase reverse transcriptase.
GN      TERT-1.
OS      Euplotes crassus.
OC      Eukaryota; Alveolata; Ciliophora; Spirotrichea; Hypotrichia;
OC      Euplotida; Euplotidae; Moneuplotes.
OX      NCBI_TaxID=5936;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Wang L., Dean S.R., Shippen D.E.;
RT      "Oligomerization of the Telomerase Reverse Transcriptase from B. crassus.";
RL      Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF528527; AAM95622.1; -.
DR      GO: GO:0005634; C:nucleus; IEA.
DR      GO: GO:0003677; F:DNA binding; IEA.
DR      GO: GO:0003723; F:RNA binding; IEA.
DR      GO: GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR      GO: GO:0003721; F:telomeric template RNA reverse transcriptase.
DR      GO: GO:0016740; F:transferase activity; IEA.
DR      GO: GO:0006278; P:RNA dependent DNA replication; IEA.
DR      InterPro: IPR000477; RVTse.
DR      InterPro: IPR003545; Telomerase_RT.
DR      Pfam: PF00078; rvt; 2.
DR      PRINTS; PR01365; TELOMERASERT.
DR      Rfam: RF00001; TERT.
KW      RNA-directed DNA polymerase; Transfexase.
SQ      SEQUENCE 1032 AA; 122966 MW; 0C401515839801A8 CRC64;

Query Match      8.0%; Score 474; DB 5; Length 1032;
Best Local Similarity 24.8%; Pred. NO. 1.5e-27;
Matches 152; Conservative 112; Mismatches 275; Indels 74;

Qy      483 NERRFLRNTKFIISLGKHAKLSQBLTWKMSVRDCAWLRRSPGVCVPAAAEHLFI
Db      379 NRKSFQSKIKYVGLNKHLELHKNLLGLDKIKWLI----GFETSKKNVHYFI
Qy      540 ILAKFLHLMWSVYVVELLRSFYFTTTFQKNRFFFYRKSVMSKLSQSIGIRQHJFI
Db      435 VLWRILRMIFEDVYVSLIRCFYFTEQOKSYSETYYRKNIWDIMVKYSIAD-LN
Qy      600 EL-SEAEYRQHRARPALLTSRLAPIKPDGLRIVNMDDYVGARTFR-----F
Db      494 EYKEDMDVMKKNLELFA--PGKLRLPKKTTFRIM-----TFNKKILDPE
Qy      654 LTRSRYKALFSLVINYERARR--PGLGASVLGLDDIHRAMRTFVLRVRAODPPPE
Db      543 MTNTNKLVSLSHLMKTLKNRMFKDPGFANFYNDVDMRKVEEFVLKWR-QVGRPK
Qy      711 VDMTGAYDTIPQDRL-----TEVIASIIKPNTYCVRR-----YAVVQKAAGHV
Db      602 MDIEKCYSDVDREKLSQLLGLTTLSSSEFRIMTVQAMKRNAEVDVLDKCAKNV
Qy      761 ----SHVSTILTLOQPMRFVFAHLETSPLRDVAVIEOSSINSREASSGLFDVFIRF
Db      662 QKWQKIALGEGQYPSLLNVLEDDQNDLNAXETLIVENQKEDPYKKKALLDPVIKI

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us-09-424-686f-2.rspt

RGKSYVOCQIGIPQGSILSTLLCSLCYGD MENKLFAGIRRDG-----LILLRIVD 868
NRKYYKQTKGIPQGLCVSSILSSFYASLEENALGYLRKESMDANDPNITLLMLTLD 781
LVTPHLTAKTFLRTLVRGVPEYGCVVNLRTVVNFPVEDEALG--GTAFV--QMPA 924
LITTKENNALFIEKLINVSRQNKFKFNKKLOTNFPDPSKLNKYGNASVEDQNI 841
FPWCGLLDTRTLEVOQSDYSSYARTSIRASLTFN--RGFKAGRNMRKLFEGVLRKCH 983
IDWIGISIDMSTLALMPNI--NLRRKGILCTILNMNMOTKKASMWLKRKL-----K 892
LDLQVNSLQTVCTN-----LYKILLQAYRFHACVLQLPFPQOVWKNPTFFLRVI 1036
ANNITHYPRKTIITNREFSNKTLNKLYIAGAYKMOCCEIYKDHFT--NTEHPOLD 950
ASLCYSILKA 1049
CAIIVSVTRA 963

April 22, 2004, 00:16:42

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